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OM protein - protein search, using sw model

Run on: May 30, 2006, 15:08:01 ; Search time 19.333 Seconds
(without alignments)
81.494 Million cell updates/sec

Title: US-10-758-165A-10
Perfect score: 97
Sequence: 1 VDCQKATNPYPYAPGKQ 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 271358

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, AA.*
1: /EMC_Celerra_SIDS3/prodata/2/iaa/5.COMB.pep.*
2: /EMC_Celerra_SIDS3/prodata/2/iaa/6.COMB.pep.*
3: /EMC_Celerra_SIDS3/prodata/2/iaa/7.COMB.pep.*
4: /EMC_Celerra_SIDS3/prodata/2/iaa/H.COMB.pep.*
5: /EMC_Celerra_SIDS3/prodata/2/iaa/PCUS.COMB.pep.*
6: /EMC_Celerra_SIDS3/prodata/2/iaa/RE.COMB.pep.*
7: /EMC_Celerra_SIDS3/prodata/2/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	33.0	9	2	US-09-920-262A-6
2	32	33.0	15	2	US-09-674-973A-64
3	31	32.0	11	2	US-09-307-265A-14
4	31	32.0	12	1	US-08-260-582-47
5	31	32.0	12	1	US-08-260-582-48
6	31	32.0	12	5	PCT-US95-05471-47
7	31	32.0	12	5	PCT-US95-05471-48
8	30	30.9	9	2	US-09-865-548A-126
9	30	30.9	14	2	US-09-502-426B-27
10	30	30.9	17	1	US-08-333-565-22
11	30	30.9	17	1	US-08-661-479-22
12	29	29.9	9	2	US-09-042-353-366
13	29	29.9	9	2	US-08-758-417A-214
14	29	29.9	15	2	US-08-278-774-20
15	29	29.9	18	2	US-09-856-920-1
16	28	28.9	10	2	US-09-641-803-18
17	28	28.9	10	2	US-09-641-802-18
18	28	28.9	10	2	US-09-641-801-18
19	28	28.9	10	2	US-10-281-652-18
20	28	28.9	11	1	US-07-958-903A-10
21	28	28.9	11	1	US-08-462-018-10
22	28	28.9	11	1	US-08-823-245-10
23	28	28.9	11	2	US-07-963-329A-60
24	28	28.9	11	2	US-09-318-001-10
25	28	28.9	11	2	US-09-064-159-10
26	28	28.9	11	5	PCT-US92-09443A-60

27	28	28.9	15	1	US-08-080-073-26	Sequence 26, Appl
28	28	28.9	16	2	US-10-044-708A-3	Sequence 3, Appl
29	28	28.9	18	1	US-08-084-718-30	Sequence 30, Appl
30	28	28.9	18	1	US-08-443-976-30	Sequence 30, Appl
31	28	28.9	18	1	US-08-443-977-30	Sequence 21, Appl
32	27	27.8	11	2	US-09-809-517A-21	Sequence 21, Appl
33	27	27.8	18	1	US-08-421-702A-100	Sequence 100, Appl
34	27	27.8	18	1	US-08-303-052A-100	Sequence 100, Appl
35	27	27.8	18	1	US-08-421-696A-100	Sequence 100, Appl
36	27	27.8	18	1	US-08-421-697A-100	Sequence 100, Appl
37	27	27.8	18	1	US-08-421-698A-100	Sequence 100, Appl
38	27	27.8	18	1	US-08-421-699A-101	Sequence 48, Appl
39	27	27.8	18	1	US-09-017-205-48	Sequence 48, Appl
40	27	27.8	18	1	US-09-017-205-49	Sequence 9, Appl
41	26	26.8	8	3	US-09-768-006-9	Sequence 1718, Ap
42	26	26.8	8	3	US-09-641-528B-1718	Sequence 8847, Ap
43	26	26.8	8	3	US-09-641-528B-8847	Sequence 16358, A
44	26	26.8	8	3	US-09-641-528B-16358	Sequence 23996, A
45	26	26.8	8	3	US-09-641-528B-23996	

ALIGNMENTS

RESULT 1
US-09-920-262A-6
Sequence 6, Application US/09920262A
Patent No. 6902734
GENERAL INFORMATION:
APPLICANT: Shealy, David
APPLICANT: Knight, David
APPLICANT: Scallion, Bernie
APPLICANT: Giles-Komar, Jill
TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES
FILE REFERENCE: CEN0248
CURRENT APPLICATION NUMBER: US/09/920, 262A
CURRENT FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: 60/223,358
PRIOR FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: 60/236,827
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver 3.1
SEQ ID NO 6
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-920-262A-6
Query Match 33.0%; Score 32; DB 2; Length 9;
Best Local Similarity 83.3%; Pred. No. 5e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 8 NIPYPT 13
DB 4 NIPYPT 9
RESULT 2
US-09-674-973A-64
Sequence 64, Application US/09674973A
Patent No. 6759046
GENERAL INFORMATION:
APPLICANT: No. 6759046sk Hydo ASA
TITLE OF INVENTION: Peptides
FILE REFERENCE: 26625-296
CURRENT APPLICATION NUMBER: US/09/674, 973A
CURRENT FILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 459
SOFTWARE: PatentIn version 3.0
SEQ ID NO 64
LENGTH: 15

TYPE: PRT
ORGANISM: Homo sapiens
US-09-674-973A-64

Query Match 33.0%; Score 32; DB 2; Length 15;
Best Local Similarity 54.5%; Pred. No. 1e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VDQKATNIFP 11
|:|:|:|:
Db 4 VEDQKTLVFP 14

RESULT 3
US-09-307-265A-14
Sequence 14, Application US/09307265A
Patent No. 6223456
GENERAL INFORMATION:
APPLICANT: Gu, Trent
APPLICANT: Orita, Satoshi
APPLICANT: Han, Min
TITLE OF INVENTION: RAS SUPPRESSOR SUR-5
FILE REFERENCE: UTC-03732
CURRENT APPLICATION NUMBER: US/09/307,265A
CURRENT FILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH: 11
TYPE: PRT
ORGANISM: Caenorhabditis elegans
US-09-307-265A-14

Query Match 32.0%; Score 31; DB 2; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 11 PYTAGKQ 18
|:|:|:|:
Db 1 PYTSSGKK 8

RESULT 4
US-08-260-582-47
Sequence 47, Application US/08260582
Patent No. 5635182
GENERAL INFORMATION:
APPLICANT: McCoy, John M.
APPLICANT: Lu, Zhijian
TITLE OF INVENTION: METHOD OF DETECTING LIGAND
TITLE OF INVENTION: INTERACTIONS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/260,582
FILING DATE: 16-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meinel, M. C.
REGISTRATION NUMBER: 31,544
REFERENCE/DOCKET NUMBER: GI 5236
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-260-582-47

Query Match 32.0%; Score 31; DB 1; Length 12;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 11 PYTAGKQ 18
|:|:|:|:
Db 4 PWLAPGEO 11

RESULT 5
US-08-260-582-48
Sequence 48, Application US/08260582
Patent No. 5635182
GENERAL INFORMATION:
APPLICANT: McCoy, John M.
APPLICANT: Lu, Zhijian
TITLE OF INVENTION: METHOD OF DETECTING LIGAND
TITLE OF INVENTION: INTERACTIONS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/260,582
FILING DATE: 16-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meinel, M. C.
REGISTRATION NUMBER: 31,544
REFERENCE/DOCKET NUMBER: GI 5236
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-260-582-48

Query Match 32.0%; Score 31; DB 1; Length 12;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 11 PYTAGKQ 18
|:|:|:|:
Db 4 PWLAPGEO 11

RESULT 6
PCT-US95-05471-47
; Sequence 47, Application PC/TUS9505471
; GENERAL INFORMATION:
; APPLICANT: METHOD OF DETECTING LIGAND INTERACTIONS
; TITLE OF INVENTION: 76
; NUMBER OF SEQUENCES: 76
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05471
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEITICAL: NO
; ANTI-SENSE: NO
PCT-US95-05471-47

Query Match 32.0%; Score 31; DB 5; Length 12;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 11 PYTAPGKQ 18
|:|:|:|
Db 4 PWLAPGEQ 11

RESULT 7
PCT-US95-05471-48
; Sequence 48, Application PC/TUS9505471
; GENERAL INFORMATION:
; APPLICANT: METHOD OF DETECTING LIGAND INTERACTIONS
; TITLE OF INVENTION: 76
; NUMBER OF SEQUENCES: 76
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05471
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEITICAL: NO
; ANTI-SENSE: NO
PCT-US95-05471-48

Query Match 32.0%; Score 31; DB 5; Length 12;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 11 PYTAPGKQ 18
|:|:|:|
Db 4 PWLAPGEQ 11

RESULT 8
US-09-865-548A-126
; Sequence 126, Application US/09865548A

Patent No. 6867283
; GENERAL INFORMATION:
; APPLICANT: Barnea, Elion
; APPLICANT: Beer, Ilan
; APPLICANT: Ziv, Tamir
; APPLICANT: Admon, Arie
; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECULES
; FILE REFERENCE: 01/22080
; CURRENT APPLICATION NUMBER: US/09/865,548A
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/290,958
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 126
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-865-548A-126

Query Match 30.9%; Score 30; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 NIPFY 12
|:|:|:|
Db 1 NIPFY 5

RESULT 9
US-09-502-426B-27
; Sequence 27, Application US/09502426B
; Patent No. 6987025
; GENERAL INFORMATION:
; APPLICANT: Azpiroz, Ricardo
; APPLICANT: Choe, Sungna
; APPLICANT: Feldmann, Kenneth A.
; TITLE OF INVENTION: DWF4 POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: 11696-070001
; CURRENT APPLICATION NUMBER: US/09/502,426B
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/119,657
; PRIOR FILING DATE: 1999-02-11
; PRIOR APPLICATION NUMBER: US 60/119,658
; PRIOR FILING DATE: 1999-02-11
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Heme binding domain
US-09-502-426B-27

Query Match 30.9%; Score 30; DB 2; Length 14;
Best Local Similarity 55.6%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 10 PPYAPGKQ 18
|:|:|:|
Db 5 PPRLCPGKE 13

RESULT 10
US-08-333-565-22
; Sequence 22, Application US/08333565
; Patent No. 5622852
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.

TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/333,565
FILING DATE: 31-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-333-565-22

Query Match 30.9% Score 30; DB 1; Length 17;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 PYTAG 16
Db 3 PYLAG 8

RESULT 11
US-08-661-479-22
Sequence 22, Application US/08661479
Patent No. 5834209
GENERAL INFORMATION:
APPLICANT: KORSMEYER, Stanley J.
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
TITLE OF INVENTION: REGULATOR
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,479
FILING DATE: 11-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/333,565
FILING DATE: 31-OCT-1994
ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 15726A-000700
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-661-479-22

Query Match 30.9% Score 30; DB 1; Length 17;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 PYTAG 16
Db 3 PYLAG 8

RESULT 12
US-09-042-353-366
Sequence 366, Application US/09042353
Patent No. 6255458
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 421
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,353
FILING DATE: 13-MAR-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,739

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; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/165,699
; FILING DATE: 10-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/209,741
; FILING DATE: 09-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/352,322
; FILING DATE: 07-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/544,404
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/728,463
; FILING DATE: 10-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US96/16433
; FILING DATE: 10-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/758,417
; FILING DATE: 02-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/21803
; FILING DATE: 01-DEC-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph T.
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 014643-009040US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 366:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-042-353-366

Query Match      29.9% Score 29; DB 2; Length 9;
Best Local Similarity 83.3%; Pred. No. Se+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8 NIPYPT 13
Db      4 NSFPYT 9

RESULT 13
US-08-758-417A-214
; Sequence 214, Application US/08758417A
; Patent No. 6300129
; GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
; Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 417
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/758,417A
; FILING DATE: 02-DEC-1996
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/728,463
; FILING DATE: 10-OCT-1996
; APPLICATION NUMBER: US 08/544,404
; FILING DATE: 10-OCT-1995
; APPLICATION NUMBER: US 08/352,322
; FILING DATE: 07-DEC-1994
; APPLICATION NUMBER: US 08/209,741
; FILING DATE: 09-MAR-1994
; APPLICATION NUMBER: US 08/165,699
; FILING DATE: 10-DEC-1993
; APPLICATION NUMBER: US 08/161,739
; FILING DATE: 03-DEC-1993
; APPLICATION NUMBER: US 08/155,301
; FILING DATE: 18-NOV-1993
; APPLICATION NUMBER: US 08/096,762
; FILING DATE: 22-JUL-1993
; APPLICATION NUMBER: US 08/053,131
; FILING DATE: 26-APR-1993
; APPLICATION NUMBER: US 07/990,860
; FILING DATE: 16-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Serafini, Andrew T.
; REGISTRATION NUMBER: 41,303
; REFERENCE/DOCKET NUMBER: 014643-009030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 214:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 214:
; US-08-758-417A-214

Query Match      29.9% Score 29; DB 2; Length 9;
Best Local Similarity 83.3%; Pred. No. Se+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      8 NIPYPT 13
Db      4 NSFPYT 9

RESULT 14
US-08-278-774-20
; Sequence 20, Application US/08278774
; Patent No. 6653450
; GENERAL INFORMATION:
; APPLICANT: Berg, Richard A
; Applicant: Tomam, David P
; APPLICANT: Wallace, Donald
; TITLE OF INVENTION: MUTATED RECOMBINANT COLLAGENS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: COLLAGEN CORPORATION
; STREET: 2500 Faber Place
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: US/08/278,774
 FILING DATE: 22-JUL-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Katalyko, Katchi L
 REGISTRATION NUMBER: 36,644
 REFERENCE/DOCKET NUMBER: 94-018
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 354-4642
 TELEFAX: (415) 354-4752
 TELEX:
 INFORMATION FOR SEQ ID NO: 20:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 15 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-278-774-20

Query Match 29.9%; Score 29; DB 2; Length 15;
 Best Local Similarity 41.7%; Pred. No. 3.2e+02;
 Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 VDGQKATNIFPY 12
 : |||||
 Db 2 IGGEKAGGPAPY 13

RESULT 15
 US-09-856-920-1
 ; Sequence 1, Application US/09856920
 ; Patent No. 6740325
 ; GENERAL INFORMATION:
 ; APPLICANT: Yeda Research and Development Co.
 ; TITLE OF INVENTION: Peptide-based vaccine for influenza
 ; FILE REFERENCE: 9822 PCT
 ; CURRENT APPLICATION NUMBER: US/09/856,920
 ; CURRENT FILING DATE: 2002-02-19
 ; NUMBER OF SEQ ID NOS: 9
 ; SOFTWARE: Patentin Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 18
 ; TYPE: PRT
 ; ORGANISM: Influenza virus
 US-09-856-920-1

Query Match 29.9%; Score 29; DB 2; Length 18;
 Best Local Similarity 44.4%; Pred. No. 3.9e+02;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 7 TNIFPYTAP 15
 : |||||
 Db 5 SNCYFYDVP 13

Search completed: May 30, 2006, 15:09:26
 Job time : 20.3333 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 30, 2006, 15:04:28 ; Search time 12 Seconds
(without alignments)
144.325 Million cell updates/sec

Title: US-10-758-165A-11

Perfect score: 96
Sequence: 1 IDGQKVDPPQHGVLKQ 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3215

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*

1: Dirl:.*
2: Dirl:.*
3: Dirl:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	26.0	14	2	A56632
2	24	25.0	15	2	PT0090
3	24	25.0	18	2	A61577
4	23	24.0	11	1	GMROL
5	23	24.0	11	2	A60656
6	23	24.0	16	2	D96655
7	23	24.0	16	2	C90981
8	23	24.0	16	2	A65827
9	23	24.0	18	2	S70340
10	22	22.9	9	2	B39841
11	22	22.9	11	2	A33917
12	22	22.9	18	2	S29379
13	21	21.9	7	2	A34818
14	21	21.9	14	2	PC7075
15	21	21.9	15	2	A30330
16	21	21.9	16	2	A49226
17	21	21.9	17	2	A65274
18	21	21.9	17	2	G85956
19	21	21.9	18	2	I55453
20	21	21.9	18	2	H75063
21	20	20.8	10	2	S33844
22	20	20.8	10	2	I48778
23	20	20.8	10	2	G60589
24	20	20.8	12	2	S68402
25	20	20.8	12	2	S68271
26	20	20.8	12	2	PM0170
27	20	20.8	13	2	S23640
28	20	20.8	13	2	S47357
29	20	20.8	13	2	S47358

30	20	20.8	14	2	PC4382
31	20	20.8	14	2	P00152
32	20	20.8	15	2	S51735
33	20	20.8	15	2	B49655
34	20	20.8	15	2	PH0789
35	20	20.8	15	2	S71306
36	20	20.8	16	2	B49255
37	20	20.8	16	2	F49039
38	20	20.8	18	2	D49570
39	19.5	20.3	17	2	B36727
40	19	19.8	11	2	A40693
41	19	19.8	11	2	PC2173
42	19	19.8	11	2	J02307
43	19	19.8	14	2	C35141
44	19	19.8	14	2	S27140
45	19	19.8	15	2	S14749

ALIGNMENTS

RESULT 1

A56632 neosulfakinin-II - flesh fly (Sarcophaga bullata)

N:Alternate names: Neb-SK-II

N:Contains: neosulfakinin-I (Neb-SK-I)

C:Species: Sarcophaga bullata

C>Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004

C:Accession: A56632

R:Fonagy, A.; Schoofs, L.; Proost, P.; Van Damme, J.; De Loof, A.

Comp. Biochem. Physiol. C 103, 135-142, 1992

A>Title: Isolation and primary structure of two sulfakinin-like peptides from the fleshf

A:Reference number: A56632; MUID:93083101; PMID:1360367

A:Accession: A56632

A:Molecule type: protein

A:Residues: 1-14 <FON>

A:Cross-references: UNIPROT:P41493; UNIPARC:UPI000013054D

A:Experimental source: heads

A>Note: sequence extracted from NCBI backbone (NCBI:120391)

C:Keywords: amidated carboxyl end; neuropeptide; sulfoprotein

F:1-14/Product: neosulfakinin-II #status experimental <NSK2>

F:6-14/Product: neosulfakinin-I #status experimental <NSK1>

F:9/Binding site: sulfate (Tyr) (covalent) #status predicted

F:14/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 26.0%; Score 25; DB 2; Length 14;

Best Local Similarity 50.0%; Pred. No. 6.1e+02;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 DEQPPQHG 14
Db 3 EEQPDYDG 10

RESULT 2

PT0090 alpha-glucosidase (EC 3.2.1.20) - honeybee (fragment)

C:Species: Apis mellifera (honeybee)

C>Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004

C:Accession: PT0090

R:Kimura, A.; Takata, M.; Fukushi, Y.; Mori, H.; Matsui, H.; Chiba, S.

Biosci. Biotechnol. Biochem. 61, 1091-1098, 1997

A>Title: A catalytic amino acid and primary structure of active site in Aspergillus nige

A:Reference number: PT0090; MUID:9739878; PMID:9255970

A:Molecule type: protein

A:Residues: 1-15 <KIM>

A:Cross-references: UNIPROT:Q7M3M5; UNIPARC:UPI000017BF08

C:Keywords: glycosidase; hydrolase

Query Match 25.0%; Score 24; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 9.9e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 IDGQKVD 7
||| :||
Db 2 IDGFRID 8

RESULT 3

A:Accession: A61577
A:Title: Two new extracellular serine proteases from Streptomyces fradiae.
A:Reference number: A61577; MUID:92155439; PMID:1786859
A:Accession: A61577
A:Molecule type: protein
A:Residues: 1-18 <SIN>
A:Cross-references: UNIPROT:Q7M198; UNIPARC:UPI000017AE13
C/Keywords: extracellular protein; hydrolase; serine proteinase

Query Match 25.0%; Score 24; DB 2; Length 18;
Best Local Similarity 27.3%; Pred. No. 1.2e+03;
Matches 3; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 IDGQKVDGFP 11
:|:|:
Db 2 VGGTRAAQDFP 12

RESULT 4

leucosulfakinin - Madeira cockroach

N:Alternate names: LSK
C/Species: Leucophaea madeire (Madeira cockroach)
C/Date: 17-Mar-1997 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
C/Accession: A01622
R:Nachman, R.J.; Holman, G.M.; Haddon, W.F.; Ling, N.
Science 234, 71-73, 1986
A:Title: Leucosulfakinin, a sulfated insect neuropeptide with homology to gastrin and ch
A:Reference number: A01622; MUID:86315858; PMID:3749893
A:Accession: A01622
A:Molecule type: protein
A:Residues: 1-11 <NAC>
A:Cross-references: UNIPROT:P04428; UNIPARC:UPI000012E960
C/Keywords: gastrin
C/Binding site: sulfate (Tyr) (covalent) #status experimental
F:11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 24.0%; Score 23; DB 1; Length 11;
Best Local Similarity 57.1%; Pred. No. 1e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 8 EQFPONG 14
||| :|
Db 1 EQFEDYG 7

RESULT 5

A:Accession: A60656
A:Title: Isolation and structure of two gastrin/CK-1-like neuropeptides from the American
A:Reference number: A60656; MUID:50137190; PMID:2615921
A:Accession: A60656
A:Molecule type: protein
A:Residues: 1-11 <VEE>

A:Cross-references: UNIPROT:P36885; UNIPARC:UPI000012E962
C/Comment: This neuropeptide stimulates hindgut contractions.
C/Keywords: amidated carboxyl end; neuropeptide; sulfoprotein
F:6/Binding site: sulfate (Tyr) (covalent) #status experimental
F:11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 24.0%; Score 23; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 1e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 8 EQFPONG 14
||| :|
Db 1 EQFDDYG 7

RESULT 6

A:Accession: D49655
A:Title: Dominant T-cell-receptor beta chain variable region V beta 14+ clones in juveni
A:Reference number: A49655; MUID:94068553; PMID:8248215
A:Accession: D49655
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-16 <GRO>
A:Cross-references: UNIPARC:UPI000017C3CA
A:Experimental source: peripheral blood lymphocytes
A:Note: sequence extracted from NCBI backbone (NCBI:P:140448)
C/Keywords: T-cell receptor

Query Match 24.0%; Score 23; DB 2; Length 16;
Best Local Similarity 55.6%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 DGQKVDGFP 10
||| :|||
Db 7 DRAPVNEQF 15

RESULT 7

A:Accession: C90981
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: C90981
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-16 <HAY>
A:Cross-references: UNIPROT:Q8X8T5; UNIPARC:UPI000000D08D2; GB:BA000007; PIDN:BA836242.1;
A:Experimental source: strain O157:H7, substrain RMD 0509952
C/Genetics:
A:Gene: EC62819

Query Match 24.0%; Score 23; DB 2; Length 16;
Best Local Similarity 80.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 9 QPQKH 13
||| :||
Db 5 QPKQH 9

RESULT 8

A85827
his operon leader peptide [imported] - *Escherichia coli* (strain O157:H7, substrain EDL93)
C/Species: *Escherichia coli*
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C/Accession: A85827
R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A/Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
A/Reference number: A85480; MUID:21074935; PMID:11206551
A/Accession: A85827
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-16 <STO>
A/Cross-references: UNIPROT:Q8X8T5, UNIPARC:UPI00000D08D2, GB:AEO05174, NID:912516199, F
A/Experimental source: strain O157:H7, substrain EDL933
C/Genetics:
A/Gene: hlaB

Query Match 24.0%; Score 23; DB 2; Length 16;
Best Local Similarity 80.0%; Pred. No. 1.6e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 QFPOH 13
Db 5 QFQKH 9

RESULT 9

S70340
napin large chain L1A - Swedish turnip (fragments)
C/Species: *Brassica napus* var. *rapifera* (Swedish turnip, rutabaga)
C/Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 31-Dec-2004
C/Accession: S70340
R/Neumann, G.M.; Condron, R.; Thomas, I.; Polya, G.M.
Biochim. Biophys. Acta 1295, 34-43, 1996
A/Title: Purification and sequencing of multiple forms of *Brassica napus* seed napin larg
A/Reference number: S70340; MUID:96283791; PMID:8679671
A/Accession: S70340
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-12,13-18 <NEU>
A/Cross-references: UNIPROT:Q39344; UNIPROT:Q9S9F0; UNIPARC:UPI000017B02E; UNIPARC:UPI00
C/Superfamily: Alpha amylase inhibitor

Query Match 24.0%; Score 23; DB 2; Length 18;
Best Local Similarity 36.4%; Pred. No. 1.8e+03;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 QKVDQFPHG 14
Db 1 QOIQQGQGG 11

RESULT 10

B39841
dextranucrase (EC 2.4.1.5) - *Streptococcus sobrinus* (fragment)
C/Species: *Streptococcus sobrinus*
C/Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 09-Jul-2004
C/Accession: B39841
R/Mooser, G.; Helfa, S.A.; Paxton, R.J.; Shively, J.E.; Lee, T.D.
J. Biol. Chem. 266, 8916-8922, 1991
A/Title: Isolation and sequence of an active-site peptide containing a catalytic aspart
A/Reference number: A39841; MUID:91224988; PMID:1827439
A/Accession: B39841
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-9 <MOO>
A/Cross-references: UNIPROT:Q7M0L7, UNIPARC:UPI000017AC69
C/Keywords: glycosyltransferase; hexosyltransferase

Query Match 22.9%; Score 22; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 DGQVD 7
Db 1 DGVRVD 6

RESULT 11

A33917
dihydroorotase (EC 3.5.2.3) - Chinese hamster (fragment)
C/Species: *Cricetulus griseus* (Chinese hamster)
C/Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 07-Nov-1997
C/Accession: A33917
R/Simmer, J.P.; Kelly, R.E.; Scully, J.L.; Grayson, D.R.; Rinker Jr., A.G.; Bergh, S.T.;
Proc. Natl. Acad. Sci. U.S.A. 86, 4382-4386, 1989
A/Title: Mammalian aspartate transcarbamylase (ATCase): sequence of the ATCase domain and
A/Reference number: A33917; MUID:89282776; PMID:2543974
A/Accession: A33917
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-11 <SIM>
A/Cross-references: UNIPARC:UPI0000176037; GB:M23652
C/Superfamily: rudimentary enzyme; aspartate(ornithine carbamoyltransferase homology; Bac
arabamoyl-phosphate synthase (glutamine-hydrolyzing) large chain homology; carbamoyl-phos
C/Keywords: hydrolase

Query Match 22.9%; Score 22; DB 2; Length 11;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DGQKV 6
Db 2 EQQKV 6

RESULT 12

S29379
sorbitol dehydrogenase - sheep
C/Species: *Ovis orientalis aries*, *Ovis ammon aries* (domestic sheep)
C/Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 09-Jul-2004
C/Accession: S29379
R/Retersen, H.; Sletten, K.; McKinley-McKee, J.S.
Eur. J. Biochem. 211, 861-869, 1993
A/Title: Affinity labelling of sorbitol dehydrogenase from sheep liver with alpha-bromo-
A/Reference number: S29379; MUID:93170323; PMID:8436142
A/Accession: S29379
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-18 <RBI>
A/Cross-references: UNIPROT:Q9TR15; UNIPARC:UPI0000087DC1
C/Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology

Query Match 22.9%; Score 22; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 2.7e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 DEQFPHG 14
Db 10 DVHYQHG 17

RESULT 13

A34818
vicillin 72K chain - pigeon pea (fragment)
C/Species: *Cajanus cajan* (pigeon pea)
C/Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 30-Sep-1993
C/Accession: A34818
R/Mawal, Y.R.; Mawal, M.R.; Ranjekar, P.K.
Biochem. Biophys. Res. Commun. 166, 1446-1452, 1990
A/Title: Unusual denaturation properties of vicillin from *Cajanus cajan*.
A/Reference number: A34818; MUID:90165956; PMID:2306256
A/Accession: A34818
A/Status: preliminary

A:Molecule type: protein
 A:Residues: 1-7 <MM>
 A:Cross-references: UNIPARC:UPI000017B040

Query Match 21.9%; Score 21; DB 2; Length 7;
 Best Local Similarity 42.9%; Pred. No. 2.8e+05;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 GQKVDQ 9
 | : | : | :
 Db 1 GARVDQ 7

RESULT 14

PC7075
 guanylate cyclase (EC 4.6.1.2), soluble, alpha-1 chain - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
 C/Accession: PC7075
 R/Taughta, A.; Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Matsui, T.; Watanabe, Y.;
 Electrophoresis 21, 1853-1871, 2000
 A/Title: Proteome analysis of mouse brain: Two-dimensional electrophoresis profiles of p
 A/Reference number: PC7072
 A/Accession: PC7075
 A:Molecule type: protein
 A:Residues: 1-14 <TSU>
 A:Cross-references: UNIPROT:Q7M058; UNIPARC:UPI000017C675
 A/Experimental source: Strain C57BL/6Ct Slc, male; brain, striatum
 C/Keywords: brain; phosphorus-oxygen lyase

Query Match 21.9%; Score 21; DB 2; Length 14;
 Best Local Similarity 50.0%; Pred. No. 3e+03;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 KVDEQFPQ 12
 | : | : | :
 Db 3 KVGDAIPQ 10

RESULT 15

A30330
 neuropeptide pep - California sea hare
 C/Species: Aplysia californica (California sea hare)
 C/Date: 02-Feb-1990 #sequence_revision 02-Feb-1990 #text_change 09-Jul-2004
 C/Accession: A30330
 R/Lloyd, P.E.; Connolly, C.M.;
 U. Neurosci. 9, 312-317, 1989
 A/Title: Sequence of pedal peptide: a novel neuropeptide from the central nervous system
 A/Reference number: A30330; MUID:89110403; PMID:2913209
 A/Accession: A30330
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-15 <LLO>
 A:Cross-references: UNIPROT:Q7M3P8; UNIPARC:UPI000017BD9A
 C/Keywords: neuropeptide

Query Match 21.9%; Score 21; DB 2; Length 15;
 Best Local Similarity 30.0%; Pred. No. 3.2e+03;
 Matches 3; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 6 VDEQFPQHL 15
 : | : | : | :
 Db 2 LDSVYGTHGM 11

Search completed: May 30, 2006, 15:08:20
 Job time : 13 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 30, 2006, 15:01:11 ; Search time 68.6667 Seconds
(without alignments)
242.480 Million cell updates/sec

Title: US-10-758-165A-11
Perfect score: 96
Sequence: 1 IDGQKVDQFPQHGLVKQ 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 12648

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 7.2: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	31.2	16	2	Q7RPP5_PLAYO
2	29	30.2	13	2	Q9UPB7_HUMAN
3	28	29.2	14	2	Q9JUN5_MOUSE
4	28	29.2	18	2	Q8QFT3_CHICK
5	25	26.0	14	1	NSK2_SARBU
6	25	26.0	15	1	COX5A_SCVCA
7	25	26.0	18	2	O12692_9PLVG
8	24	25.0	15	2	Q7M3W5_APTME
9	24	25.0	15	2	Q9R563_ECOLI
10	24	25.0	18	2	Q4YLT9_PLABE
11	24	25.0	18	2	Q5FBR5_SUNMU
12	24	25.0	18	2	Q7M198_STRFR
13	23	24.0	11	1	LSK1_LEBMA
14	23	24.0	11	1	LSKP_PBRAM
15	23	24.0	14	2	P78359_HUMAN
16	23	24.0	15	1	CX1B_CONBE
17	23	24.0	16	1	LPHI_CONBE
18	23	24.0	18	2	O13167_XIPGL
19	22	22.9	9	2	Q7M0L7_GSTRE
20	22	22.9	10	2	Q5D4Q4_PRHOO
21	22	22.9	11	2	Q48933_MYCBO
22	22	22.9	11	2	Q79C20_MYCBO
23	22	22.9	11	2	Q79C22_MYCTU
24	22	22.9	13	2	Q39380_BRAOL
25	22	22.9	13	2	Q38ZP8_LACSS
26	22	22.9	15	1	ODP3_SOLTU
27	22	22.9	16	2	Q9TRHO_BOVIN
28	22	22.9	18	1	RL24_PROVU
29	22	22.9	18	2	Q4XFY5_PLACH
30	22	22.9	18	2	Q580R2_GTRYP
31	22	22.9	18	2	Q9TR15_SHEEP

ALIGNMENTS

```

RESULT 1
ID Q7RPP5_PLAYO PRELIMINARY; PRT; 16 AA.
AC Q7RPP5;
DT 15-DEC-2003, integrated into UniProtKB/TREMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Hypothetical protein.
GN ORFNames=EY01411;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=1YXNL;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angiuoli S.V., Suh B.B., Kooij T.W., Pertea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shalom S.J., van Aken S.B., Riedmiller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabli A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Valdivia A.B.,
RA van Lin L.H., Jense C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RA "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii."
RL Nature 419:512-519(2002).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL, AABL01000372; EAA20742.1; -; Genomic_DNA.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 16 AA; 1778 MW; 22142D3BC2EE109 CRC64;

Query Match 31.2%; Score 30; DB 2; Length 16;
Best Local Similarity 62.5%; Pred. No. 1.6e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 IDGQKXDE 8
|:|:|:|
Db 4 INGSKIDE 11

RESULT 2
ID Q9UPB7_HUMAN PRELIMINARY; PRT; 13 AA.
AC Q9UPB7;
DT 01-MAY-2000, integrated into UniProtKB/TREMBL.

```

DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Inosine monophosphatase 2 (Fragment).
GN Name=IMP2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97463449; PubMed=9322233; DOI=10.1038/sj.mp.4000325;
RA Yoshikawa T., Turner G., Esterling L.E., Sanders A.R.,
RA Defera-Madleigh S.D.;
RT "A novel human myo-inositol monophosphatase gene, IMP.18p, maps to a
RT susceptibility region for bipolar disorder.";
RL Mol. Psychiatry 2:393-397(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20284187; PubMed=10822344; DOI=10.1038/sj.mp.4000688;
RA Yoshikawa T., Padigar M., Karkera J.D., Sharma M., Berrettini W.H.,
RA Esterling L.E., Defera-Madleigh S.D.;
RT "Genomic structure and novel variants of myo-inositol monophosphatase
RT 2.";
RL Mol. Psychiatry 5:165-171(2000).
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CC
DR EMBL; AF025882; AAD22136.1; -; Genomic_DNA.
DR EMBL; AF025881; AAD22136.1; JOINED; Genomic_DNA.
FT NON_TER 1 1
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1589 MW; F3415D841F48D401 CRC64;
Query Match 30.2%; Score 29; DB 2; Length 13;
Best Local Similarity 36.4%; Pred. No. 1.8e+03;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 8 DEQFPGHGLVKQ 18
Db 1 ERFPSHRFIAE 11
RESULT 3
OSJUS MOUSE
ID OSJUS_MOUSE PRELIMINARY; PRT; 14 AA.
AC OSJUS;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE B-Raf protein (Fragment).
GN Name=B-raf;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Barnier J.V., Papin C., Eychene A., Lecocq O.;
RT "The mouse B-raf gene encodes multiple protein isoforms with tissue-
RT specific expression.";
RL J. Biochem. 270:23381-23389(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Barnier J.V.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
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CC
DR EMBL; AJ276308; CAB81556.1; -; mRNA.

DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:0005634; C:nucleus; RCA.
DR GO; GO:0005886; C:plasma membrane; IDA.
DR GO; GO:0003677; F:DNA binding; RCA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; RCA.
DR GO; GO:0008270; F:zinc ion binding; RCA.
DR GO; GO:0050875; P:cellular physiological process; RCA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; RCA.
FT NON_TER 1 1
FT NON_TER 14 14
SQ SEQUENCE 14 AA; 1748 MW; D1E0505C44927F02 CRC64;
Query Match 29.2%; Score 28; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 2.9e+03;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 7 DEQFPGHGLVKQ 18
Db 1 DEKPEVELDDQ 12
RESULT 4
ID OSQFT3_CHICK PRELIMINARY; PRT; 18 AA.
AC OSQFT3;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Sterol regulatory element binding protein 1 (Fragment).
GN Name=SREBP-1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Asaef S., Pitel F., Morrison M., Alizadeh M., Gondret F., Diot C.,
RA Leclercq B., Vignal A., Douaire M., Lagarrigue S.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
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CC
DR EMBL; AJ441122; CAD29619.1; -; Genomic_DNA.
FT NON_TER 1 1
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 1947 MW; 3206A67750EFD7EA CRC64;
Query Match 29.2%; Score 28; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 3.8e+03;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 7 DEQFPGHGLVKQ 18
Db 1 DSPLCNHGKVKQ 12
RESULT 5
ID NSK2_SARBU STANDARD; PRT; 14 AA.
AC P41493;
DT 01-NOV-1995, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1995, sequence version 1.
DT 07-MAR-2006, entry version 32.
DE Neosulfakinin-2 (Neosulfakinin-II) (Neb-SK-II).
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga; Neobellieria.
OX NCBI_TaxID=7385;
RN [1]
RP PROTEIN SEQUENCE.

CC TISSUE=Head;
 RX MEDLINE=93083101; PubMed=1360367;
 RA Fonagy A., Schoofs L., Proost P., van Damme J., de Loof A.;
 RT "Isolation and primary structure of two sulfakinin-like peptides from
 the fleshfly, *Nobeliella bullata*.";
 RL Comp. Biochem. Physiol. 103C:135-142(1992).
 CC -1- FUNCTION: Myotropic peptide.
 CC -1- SUBCELLULAR LOCATION: Secreted protein.
 CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
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 CC -----
 DR PIR: A56632; A56632.
 DR InterPro: IPR013152; Gastrin_CCK.
 DR InterPro: IPR013259; Sulfakinin.
 DR Pfam: PF08257; Sulfakinin; 1.
 DR PROSITE: PS00259; GASTRIN; 1.
 KM Annotation: Direct protein sequencing; Neuropeptide; Sulfation.
 FT PEPTIDE 1 14
 FT Neosulfakinin-2.
 FT /FTid=PRO_0000043897.
 FT MOD_RES 9 9
 FT Sulfotyrosine (Potential).
 FT MOD_RES 14 14
 FT Phenylalanine amide (Potential).
 SQ SEQUENCE 14 AA; 1796 MW; 8B4E06D5B61C62AA CRC64;
 Query Match 26.0%; Score 25; DB 1; Length 14;
 Best Local Similarity 50.0%; Pred. No. 9.2e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 7 DEOPPHG 14
 Db 3 EEPFDYD 10
 RESULT 6
 COX5A SCYCA STANDARD; PRT; 15 AA.
 AC P83012;
 DT 29-MAR-2005, integrated into UniProtKB/Swiss-Prot.
 DT 01-OCT-2001, sequence version 1.
 DT 07-FEB-2006, entry version 15.
 DE Cytochrome c oxidase polypeptide Va, mitochondrial (EC 1.9.3.1)
 DE (Fragment).
 OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Chondrichthyes;
 OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;
 OC Scyliorhinidae; Scyliorhinus.
 OX NCBI_TaxID=7830;
 RN [1]
 RP PROTEIN SEQUENCE.
 RC TISSUE=Rectal gland;
 RX MEDLINE=2153426; PubMed=11676495; DOI=10.1006/bbrc.2001.5826;
 RA Schummers Stekhoven F.M.A.H., Plik G., Wendelaar Bonga S.E.;
 RT "N-terminal sequences of small ion channels in rectal glands of
 sharks: a biochemical hallmark for classification and phylogeny?";
 RL Biochem. Biophys. Res. Commun. 288:670-675(2001).
 CC -1- FUNCTION: This is the heme A-containing chain of cytochrome c
 oxidase, the terminal oxidase in mitochondrial electron transport.
 CC -1- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
 c + 2 H(2)O.
 CC -1- SUBCELLULAR LOCATION: Mitochondrion, mitochondrial inner membrane.
 CC -1- SIMILARITY: Belongs to the cytochrome c oxidase Va family.
 CC -----
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 CC -----
 DR GO: 0005739; C-mitochondrion; IDA.
 DR InterPro: IPR003204; Cyt_c-ox5a.
 DR Pfam: PF02284; COX5A; 1.
 KM Direct protein sequencing; Heme; Inner membrane; Iron; Membrane;
 KM Metal-binding; Mitochondrion; Oxidoreductase.
 FT CHAIN 1 >15
 FT Cytochrome c oxidase polypeptide Va.
 FT /FTid=PRO_0000195215.

FT NON TER 15 15
 SQ SEQUENCE 15 AA; 1720 MW; 937518D750B35C5 CRC64;
 Query Match 26.0%; Score 25; DB 1; Length 15;
 Best Local Similarity 57.1%; Pred. No. 9.8e+03;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 4 QKDEOF 10
 Db 5 QETDEEF 11
 RESULT 7
 O12692_9PLVG PRELIMINARY; PRT; 18 AA.
 ID O12692_9PLVG
 AC O12692;
 DT 01-JUL-1997, integrated into UniProtKB/TrEMBL.
 DT 01-JUL-1997, sequence version 1.
 DT 07-MAR-2006, entry version 26.
 DE Gag polyprotein (Fragment).
 DE Name=gag;
 OS Simian-Human immunodeficiency virus.
 OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
 OC Lentiviruses; Primate lentivirus group.
 OX NCBI_TaxID=57667;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=SHIVku1;
 RX MEDLINE=97312452; PubMed=9168893; DOI=10.1006/viro.1997.8534;
 RA Stephens E.B., Mukherjee S., Sahni M., Zhuge W., Raghavan R.,
 RA Singh D.K., Leung K.K., Atkinson R.B., Li Z., Joag S.V., Liu Z.Q.,
 RA Narayan O.;
 RT "A cell-free stock of simian-human immunodeficiency virus that causes
 AIDS in pig-tailed macaques has a limited number of amino acid
 substitutions in both SIVmac and HIV-1 regions of the genome and has
 offered cytotropism.";
 RT Virology 231:313-321(1997).
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 CC -----
 DR EMBL: U89249; AAC57878.1; -; Genomic DNA.
 DR GO: 0019013; C:Viral nucleocapsid; IBA.
 DR GO: 0005198; F:Structural molecule activity; IBA.
 DR InterPro: IPR000071; Imm_lenv_matrix.
 DR Pfam: PF00540; Gag_p17; 1.
 KM Polypeptide.
 FT NON TER 18 18
 SQ SEQUENCE 18 AA; 1961 MW; E064725D22E62EB CRC64;
 Query Match 26.0%; Score 25; DB 2; Length 18;
 Best Local Similarity 50.0%; Pred. No. 1.2e+04;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 IDGQKVD 8
 Db 8 LSGKAD 15
 RESULT 8
 O7M3M5_APIME PRELIMINARY; PRT; 15 AA.
 ID O7M3M5_APIME
 AC O7M3M5;
 DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
 DT 15-DEC-2003, sequence version 1.
 DT 07-FEB-2006, entry version 6.
 DE Alpha-glucosidase (EC 3.2.1.20) (Fragment).
 OS Apis mellifera (Honeybee).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
 OC Apidae; Apis.
 OX NCBI_TaxID=7460;
 RN [1]

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RP PROTEIN SEQUENCE.
RX MEDLINE=97399878; PubMed=9255970;
RA Kimura A., Takara M., Fukushi Y., Mori H., Matsui H., Chiba S.;
RT "A catalytic amino acid and primary structure of active site in
RL Asepyllus niger alpha-glucosidase."
CC Biosci. Biotechnol. Biochem. 61:1091-1098(1997).
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CC -----
CC PIR; PT0090; PT0090.
DR GO; GO:0004558; F:alpha-glucosidase activity; IEA.
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1686 MW; 85730BA8387CB741 CRC64;

Query Match 25.0%; Score 24; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 1.4e+04;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 IDGOKVD 7
Db 2 IDGFRID 8

RESULT 9
Q9RS63_ECOLI PRELIMINARY; PRT; 15 AA.
ID Q9RS63_ECOLI
AC Q9RS63;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE 40 kDa porin homolog (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OC NCBI_TaxID=562;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=93328296; PubMed=8392972;
RA Dyrco M., Sori R., Cockerill F.III, De Azavedo J., Louie M.,
RT Brunton J., Sherman P.;
RT "Multiple determinants of verotoxin-producing Escherichia coli O157:H7
RT attachment-effacement."
RL Infect. Immun. 61:3382-3391(1993).
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CC -----
SQ SEQUENCE 15 AA; 1699 MW; 2767AC9298F8754D CRC64;

Query Match 25.0%; Score 24; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.4e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 DGOKVD 7
Db 7 DGNKLD 12

RESULT 10
Q4YL79_PLABE PRELIMINARY; PRT; 18 AA.
ID Q4YL79_PLABE
AC Q4YL79;
DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Hypothetical protein (Fragment).
GN ORFNames=PB400723.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OC NCBI_TaxID=5821;
RN [1]

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```

RP NUCLEOTIDE SEQUENCE.
RX PubMed=15637271; DOI=10.1126/science.1103717;
RA Hall M., Karras M., Raine J.D., Carlton J.M., Kooji T.W.A.,
RA Bettman M., Florens L., Janssen C.S., Pain A., Christopoulos G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.M.,
RA Quail M.A., Ormond D., Doggett J., Truman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R. III,
RA Kafatos F.C., Janse C.J., Barrall B.G., Turner C.M.R., Waters A.P.,
RA Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses."
RL Science 307:82-86(2005).
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; CAI01003787; CAI01022.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 18 AA; 2206 MW; EBBABA563A3085A7 CRC64;

Query Match 25.0%; Score 24; DB 2; Length 18;
Best Local Similarity 30.0%; Pred. No. 1.7e+04;
Matches 3; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 9 QPQGLVKQ 18
Db 1 KFPKYSMMHQ 10

RESULT 11
Q5FBR5_SUNMU PRELIMINARY; PRT; 18 AA.
ID Q5FBR5_SUNMU
AC Q5FBR5;
DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.
DT 15-MAR-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Thiorodoxin (Fragment).
GN Name=TXN;
OS Suncus murinus (House shrew) (Musk shrew).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Insectivora; Soricidae;
OC Crocidurinae; Suncus.
OC NCBI_TaxID=9378;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=TKU, WZ, and BAN; TISSUE=Kidney;
RX PubMed=15897627; DOI=10.1538/expanim.54.173;
RA Adjel S., Sato A., Tanaka S., Kobayashi E., Tanaka K., Namioka T.,
RA Ishikawa A.;
RT "Development and characterization of CATS markers for genetic linkage
RT mapping in the house musk shrew, Suncus murinus."
RL Exp. Anim. 54:173-180(2005).
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CC -----
DR EMBL; AB167758; BAD89500.1; -; Genomic_DNA.
DR EMBL; AB167757; BAD89499.1; -; Genomic_DNA.
DR EMBL; AB167756; BAD93380.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 18 AA; 2020 MW; D0B5FC66463A90F8 CRC64;

Query Match 25.0%; Score 24; DB 2; Length 18;
Best Local Similarity 83.3%; Pred. No. 1.7e+04;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GOKYDE 8
Db 3 GOKYDE 8

```

Db 8 GCKVGE 13

RESULT 12

Q7M198 STRFR PRELIMINARY; PRT; 18 AA.

AC 07M198; Integrated into UniProtKB/TrEMBL.

DT 15-DEC-2003, sequence version 1.

DT 07-FEB-2006, entry version 7.

DE 24k serine proteinase (EC 3.4.21.-) (Fragment).

OS Streptomyces fradiae.

OC Bacteria; Actinobacteria; Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.

NCBI_TaxID=1906;

OX NCBI_TaxID=1906;

RN [1]

RP PROTEIN SEQUENCE.

RX MEDLINE=9215439; PubMed=1786859; DOI=10.1016/0020-711X(91)90133-8; Srinha U., Wolz S.A., Lad P.J., "Two new extracellular serine proteases from Streptomyces fradiae."; Int. J. Biochem. 23:979-984 (1991).

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CC PIR; A61577; A61577.

FT NON_TER 1

FT NON_TER 18

SQ SEQUENCE 18 AA; 2004 MW; 6D6DA167845934A5 CRC64;

Query Match 25.0%; Score 24; DB 2; Length 18;

Best Local Similarity 27.3%; Pred. No. 1.7e+04;

Matches 3; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 IDGQKVDQFP 11

Db 2 VGGTRAGDEFP 12

RESULT 13

LSK1 LEUMA STANDARD; PRT; 11 AA.

ID AC P04428; Integrated into UniProtKB/Swiss-Prot.

DT 13-AUG-1987, sequence version 1.

DT 13-AUG-1987, entry version 36.

DE Leucosulfakinin-1 (leucosulfakinin-1) (LSK-1).

OS Leucophaea maderae (Madeira cockroach).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preygotha; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea; Blaberidae; Oxyhalotinae; Leucophaea.

NCBI_TaxID=6988;

OX NCBI_TaxID=6988;

RN [1]

RP PROTEIN SEQUENCE.

RX MEDLINE=6631585; PubMed=3749893; Nechman R.J., Holman G.M., Haddon W.F., Ling N.; "Leucosulfakinin, a sulfated insect neuropeptide with homology to gastrin and cholecystokinin."; Science 234:71-73 (1986).

RT Gastrin and cholecystokinin."

RL Science 234:71-73 (1986).

CC -1- FUNCTION: Changes the frequency and amplitude of contractions of the hindgut. Inhibits muscle contraction of hindgut.

CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.

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CC PIR; A01622; GMR0L.

DR InterPro; IPR013152; Gastrin_CCK.

DR InterPro; IPR013259; Sulfakinin.

DR Pfam; PF08257; Sulfakinin; 1.

DR PROSITE; PS00259; GASTRIN; 1.

KW Amdation; Direct protein sequencing; Hormone; Sulfation.

FT PEPTIDE 1

Db 11 Leucosulfakinin-1.

FT MOD_RES 6 6 /FTID=PRO_0000043891.

FT MOD_RES 11 11 Sulfotyrosine.

SQ SEQUENCE 11 AA; 1459 MW; 7E4E0680E86B5AAB CRC64;

Query Match 24.0%; Score 23; DB 1; Length 11;

Best Local Similarity 57.1%; Pred. No. 1.5e+04;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 8 EQFPQNG 14

Db 1 EQFEDYG 7

RESULT 14

LSKP PERAM STANDARD; PRT; 11 AA.

ID AC P36885; Integrated into UniProtKB/Swiss-Prot.

DT 01-JUN-1994, sequence version 1.

DT 01-JUN-1994, entry version 29.

DE Perisulfakinin (Pea-SK-I).

OS Periplaneta americana (American cockroach).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preygotha; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea; Blattidae; Blattinae; Periplaneta.

NCBI_TaxID=6978;

OX NCBI_TaxID=6978;

RN [1]

RP PROTEIN SEQUENCE.

RX MEDLINE=90137190; PubMed=2615921; DOI=10.1016/0143-4179(89)90038-3; Venestra J.A.; "Isolation and structure of two gastrin/CCK-like neuropeptides from the American cockroach homologous to the leucosulfakinins."; Neuropeptides 14:145-149 (1989).

RT the American cockroach homologous to the leucosulfakinins."

RL Neuropeptides 14:145-149 (1989).

CC -1- FUNCTION: Stimulates hindgut contractions.

CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.

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CC PIR; A06556; A06556.

DR InterPro; IPR013152; Gastrin_CCK.

DR InterPro; IPR013259; Sulfakinin.

DR Pfam; PF08257; Sulfakinin; 1.

DR PROSITE; PS00259; GASTRIN; 1.

KW Amdation; Direct protein sequencing; Hormone; Sulfation.

FT PEPTIDE 1

FT MOD_RES 6 6 /FTID=PRO_0000043893.

FT MOD_RES 11 11 Sulfotyrosine.

SQ SEQUENCE 11 AA; 1445 MW; 8B4E0680E86B5AAB CRC64;

Query Match 24.0%; Score 23; DB 1; Length 11;

Best Local Similarity 57.1%; Pred. No. 1.5e+04;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 8 EQFPQNG 14

Db 1 EQFEDYG 7

RESULT 15

P78359_HUMAN PRELIMINARY; PRT; 14 AA.

ID AC P78359; Integrated into UniProtKB/TrEMBL.

DT 01-MAY-1997, sequence version 1.

DT 07-FEB-2006, entry version 17.

DE NF-kappa-B transcription factor p65 (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;

OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Umbilical vein;
RA Remacle J.E., Brys R., Pype S., Nelles L., Huylebroeck D.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
DR EMBL; U88316; AAB48487.1; -; mRNA.
FT NON TER 14 14
SQ SEQUENCE 14 AA; 1662 MW; 5E30458F8262F957 CRC64;

Query March 24.0%; Score 23; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 2e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 6 VDEQFP 11
: |||
Db 1 MDLFP 6

Search completed: May 30, 2006, 15:07:38
Job time : 70.6667 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using SW model

Run on: May 30, 2006, 14:59:31 ; Search time 61.6667 Seconds
(without alignments)
133.458 Million cell updates/sec

Title: US-10-758-165A-11

Perfect score: 96

Sequence: 1 IDGQKVDQFPQHGVLKQ 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 902922

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A_Geneseq_8:*
- 1: geneseqp1980s:*
 - 2: geneseqp1990s:*
 - 3: geneseqp2000s:*
 - 4: geneseqp2001s:*
 - 5: geneseqp2002s:*
 - 6: geneseqp2003as:*
 - 7: geneseqp2003bs:*
 - 8: geneseqp2004s:*
 - 9: geneseqp2005s:*
 - 10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	96	100.0	18	ADRI0611
2	78	81.2	15	ADG64569
3	36	37.5	14	ABP46438
4	36	37.5	14	ADG97265
5	36	37.5	14	AED79318
6	35	36.5	16	AEE33637
7	35	36.5	16	AEE34193
8	35	36.5	18	ADRI0610
9	34	35.4	15	AA50232
10	34	35.4	15	ABP94693
11	34	35.4	15	ABP95588
12	34	35.4	15	ABP95194
13	34	35.4	17	ADM96833
14	34	35.4	18	ADRI0609
15	33	34.4	10	ADL98126
16	33	34.4	13	ADG95486
17	33	34.4	15	ABP94247
18	33	34.4	15	ABP95554
19	33	34.4	15	ABP94098
20	33	34.4	15	ABP95117
21	33	34.4	15	ABP94539
22	33	34.4	15	ABP94780
23	33	34.4	15	ABP95372

24	33	34.4	15	ABR32079
25	33	34.4	15	ABR32127
26	33	34.4	15	ADV31901
27	33	34.4	15	ADV31853
28	33	34.4	15	AEC70956
29	33	34.4	15	AEC70908
30	33	34.4	15	AEE34208
31	33	34.4	16	AEE33641
32	32	33.3	10	AAW15125
33	32	33.3	14	AA998200
34	32	33.3	14	ABP46692
35	32	33.3	14	ABP46435
36	32	33.3	14	ADG97262
37	32	33.3	14	ADG97519
38	32	33.3	14	AED79315
39	32	33.3	14	AED79572
40	32	33.3	15	ABP95187
41	32	33.3	15	ABP94687
42	32	33.3	15	ABP94184
43	32	33.3	15	ABP94689
44	32	33.3	15	ABP95591
45	32	33.3	15	ABP95184

ALIGNMENTS

RESULT 1
ID ADR10611 standard; peptide: 18 AA.
AC ADR10611;
DT 21-OCT-2004 (first entry)
XX Horse IGE epitope recognised by monoclonal antibody 3.76, SEQ ID 11.
XX
XX Antiaethmatic; Antiallergic; Immunosuppressive; IGE; dog; asthma;
KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
KW horse.
XX
XX Equus caballus.
OS
PD
XX
XX 05-AUG-2004.
XX
XX 15-JAN-2004; 2004WO-US003566.
XX
XX 16-JAN-2003; 2003US-0440472P.
XX
XX (UTNC-) UNIV NORTH CAROLINA STATE.
XX
XX Hammerberg B;
XX
XX WPI; 2004-593545/57.
XX
XX Novel antibody that specifically binds to mammalian IGE epitope, useful
PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE
PT or treating asthma or anaphylactic shock.
XX
XX Example 6; Page 9; 14pp; English.
XX
XX The present invention relates to a novel monoclonal antibody (I) that
CC specifically binds to a mammalian IGE epitope, where the epitope is
CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
CC (I) is useful for testing an allergen reactivity of an IGE sample. The
CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
CC and corn allergens. The sample is a biological sample collected from a
CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
CC antibodies recognise epitopes on canine IGE corresponding to amino acid
CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the

CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with
 CC either pig or human epsilon-chains of IGE. The present sequence is the
 CC horse IGE 3.76 recognition site.
 CC
 XX

SQ Sequence 18 AA;

Query Match 100.0%; Score 96; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.7e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IDGQKVDQFPQHGVLVKQ 18
 |||||
 1 IDGQKVDQFPQHGVLVKQ 18

Db 1 IDGQKVDQFPQHGVLVKQ 18

RESULT 2

ADG64569
 ID ADG64569 standard; peptide; 15 AA.

AC ADG64569;

DT 18-DEC-2003 (first entry)

DE Horse immunoglobulin E, IGE, heavy chain immunogenic peptide p5.

XX Horse; immunoglobulin E; IGE; heavy chain; immunogen; allergy.

OS Equus caballus.

PN US2003087314-A1.

PD 08-MAY-2003.

PF 08-NOV-2001; 2001US-00052788.

XX 08-NOV-2001; 2001US-00052788.

PR (REGC) UNIV CALIFORNIA.

PI Gershwin LJ, Pettigrew HD, Kalina WJ;

DR WPI; 2003-765437/72.

PT Immunogenic composition comprising an isolated equine immunoglobulin E
 PT polypeptide that induces production of antibodies which specifically bind
 PT to equine immunoglobulin E.
 XX

XX Example 1; Page 8; 14pp; English.

CC The invention relates to an immunogenic composition comprising an
 CC isolated polypeptide having an amino acid sequence that is at least 80%
 CC identical to 6 (SI-56), 15 amino acid peptide sequences derived from
 CC equine immunoglobulin E (the composition induces production of an
 CC antibody that specifically binds to equine immunoglobulin (Ig)E), the six
 CC polypeptides are not explicitly identified in the specification. Also
 CC included are a composition comprising an antibody that specifically binds
 CC to a polypeptide at least 80% identical to (SI)-(56), an antibody that
 CC specifically binds to equine IGE made by the process of immunising an
 CC animal with a polypeptide at least 80% identical to (SI)-(56), making an
 CC antibody that specifically binds to equine IGE (involving immunising an
 CC animal with a composition further comprising an isolated polypeptide (the
 CC amino acid sequence of the polypeptide is at least 80% identical to (SI)-
 CC (56)), and collecting antiserum from the animal) and a kit for detection
 CC of equine IGE in a biological sample comprising the antibody and means
 CC for detecting specific binding of the antibody to equine IGE. The
 CC antibody is useful for detecting equine IGE protein in a biological
 CC sample (serum) which involves contacting the sample with the antibody,
 CC thus forming an antigen/antibody complex, and detecting the presence or
 CC absence of the antigen/antibody complex. The antibody and antigen are
 CC immobilised on a solid surface. The antibody is labelled such that the

CC complex can be detected. The complex is detected using a second labelled
 CC antibody. The peptides are useful for generating antibodies specific for
 CC IGE which can serve as a diagnostic test for allergy. The present
 CC sequence is a Horse immunoglobulin E, IGE, heavy chain immunogenic
 CC peptide from the middle portion of the C2 region.
 CC
 XX

SQ Sequence 15 AA;

Query Match 81.2%; Score 78; DB 7; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.3e-05;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IDGQKVDQFPQHG 14
 |||||
 2 IDGQKVDQFPQHG 15

Db 2 IDGQKVDQFPQHG 15

RESULT 3

ABP46438
 ID ABP46438 standard; peptide; 14 AA.

AC ABP46438;

DT 19-AUG-2002 (first entry)

DE Human Blys binding scFv VH CDR3 SEQ ID 2449.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 XX tumour necrosis factor; B cell proliferation; B cell differentiation;
 XX immunosuppressive; immunostimulant; immunomodulatory; antineutritic;
 XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 XX common variable immunodeficiency; acquired immunodeficiency syndrome.

OS Homo sapiens.

PN WO200202641-A1.

PD 10-JAN-2002.

PF 15-JUN-2001; 2001WO-US019110.

XX 16-JUN-2000; 2000US-0212210P.

PR 17-OCT-2000; 2000US-0240816P.

XX 16-MAR-2001; 2001US-0276248P.

PR 21-MAR-2001; 2001US-0277379P.

XX 25-MAY-2001; 2001US-0293499P.

XX (HUMA-) HUMAN GENOME SCI INC.

PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

DR WPI; 2002-114799/15.

PT Antibodies against B lymphocyte stimulating polypeptides, useful for the
 PT diagnosis and treatment of cancers and immune disorders.
 XX

XX Claim 2; Page 2992; 3148pp; English.

CC This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antineutritic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,

CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABB43990-ABB47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention
XX

SQ Sequence 14 AA;

Query Match 37.5%; Score 36; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 FPOHGL 15
| | | | |
Db 7 FPOHGL 12

RESULT 4
ADG97265
ID ADG97265 standard; peptide: 14 AA.

XX ADG97265;

DT 11-MAR-2004 (first entry)

XX scFv VHCDR3 peptide that immunospecifically binds BlyS SeqID 2449.

XX antibody; B lymphocyte stimulator; BlyS; tumour necrosis factor;
XX B cell proliferation; differentiation; scFv; myasthenia gravis;
XX multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
XX carcinoma; lymphoma; antineoplastic; antiarthritic; neuroprotective;
XX antiinflammatory; antiallergic; antiallergic; cytostatic.

XX Unidentified.

XX W02003055979-A2.

XX 10-JUL-2003.

XX 14-NOV-2002; 2002MO-US036496.

XX 16-NOV-2001; 2001US-0331469P.
XX 19-DEC-2001; 2001US-0340817P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
XX WPI; 2003-505530/47.

XX Novel antibody that immunospecifically binds to a B lymphocyte stimulator
XX (BlyS), useful for detecting and treating diseases or disorders e.g.
XX rheumatoid arthritis, asthma and leukemia.

XX Example 1; SEQ ID NO 2449; 394pp; English.

XX This invention relates to novel antibodies that immunospecifically bind
XX to B lymphocyte stimulator (BlyS). The BlyS gene has been mapped to
XX chromosome 13q34 and encodes a protein that is a member of the tumour
XX necrosis factor superfamily and induces both in vivo and in vitro B cell
XX proliferation and differentiation. Specifically, it refers to single
XX chain antibody molecules (scFvs) derived, preferably, from the variable
XX heavy CDR3 region that immunospecifically bind to a polypeptide, or
XX fragment thereof, of either human, murine, rat or monkey BlyS. The
XX present invention refers to the use of such antibodies in various methods
XX for the detection, diagnosis and prognosis of diseases related to the
XX aberrant expression or inappropriate function of BlyS or its receptor. As
XX such, these compositions are useful for identifying immune disorders
XX including myasthenia gravis and multiple sclerosis, inflammatory
XX disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
XX as AIDS and proliferative disorders including leukaemia, carcinoma and
XX lymphoma. Accordingly, they can be described as exhibiting various
XX activities such as antineoplastic, antiallergic, neuroprotective,
XX antiinflammatory, antiallergic, antiallergic and cytostatic. This

CC peptide sequence is a single chain antibody variable heavy CDR3 peptide
CC that immunospecifically binds BlyS of the invention.

SQ Sequence 14 AA;

Query Match 37.5%; Score 36; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 FPOHGL 15
| | | | |
Db 7 FPOHGL 12

RESULT 5
AED79318
ID AED79318 standard; peptide: 14 AA.

XX AED79318;

DT 12-JAN-2006 (first entry)

XX Human B lymphocyte binding scFv VH CDR3 peptide, SEQ ID 2449.

XX Antiinflammatory; Dermatological; Immunosuppressive; Antineoplastic;
XX Antiarthritic; Neuroprotective; Muscular-Gen.; Antiallergic;
XX Antiallergic; Anticarcinogenic; Anti-HIV; Cytostatic; B-lymphocyte;
XX antibody; autoimmune disease; B-cell lymphoma;
XX systemic lupus erythematosus; rheumatoid arthritis; immune disorder;
XX inflammation; infectious disease; hyperproliferation.

XX Homo sapiens.

XX US200525532-A1.

XX 17-NOV-2005.

XX 10-FEB-2005; 2005US-00054515.

XX 16-JUN-2000; 2000US-0212210P.
XX 17-OCT-2000; 2000US-0240816P.
XX 16-MAR-2001; 2001US-0276248P.
XX 21-MAR-2001; 2001US-0277379P.
XX 25-MAY-2001; 2001US-0293499P.
XX 15-JUN-2001; 2001US-00880748.
XX 16-NOV-2001; 2001US-0331469P.
XX 19-DEC-2001; 2001US-0340817P.
XX 14-NOV-2002; 2002US-00293418.
XX 11-FEB-2004; 2004US-0543296P.
XX 18-JUN-2004; 2004US-0580347P.

XX (RUBEN) RUBEN S. M.
XX (BARASH) BARASH S. C.
XX (CHOI) CHOI G. H.
XX (VAUGHAN) VAUGHAN T.
XX (HILBERT) HILBERT D.

XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2005-808635/82.

XX New antibodies that immunospecifically binds to B lymphocyte stimulator
XX protein, useful for diagnosing, treating, or preventing autoimmune
XX disease, e.g. systemic lupus erythematosus or rheumatoid arthritis, or B
XX cell cancer.

XX Example 1; SEQ ID NO 2449; 240pp; English.

XX The invention relates to a novel antibody that immunospecifically binds
XX to B lymphocyte stimulator protein. The protein comprises an amino acid
XX sequence that is 85% identical to the VH domain of any one of the single-
XX chain variable fragments (scFvs) of SEQ ID NOs. 1-2128, and/or an amino
XX acid sequence that is at least 85% identical to the VL domain of any one

CC of the seqs of SEQ ID NOs. 1-2128. The invention further comprises: an
CC isolated nucleic acid molecule encoding the antibody; an isolated cell
CC line that expresses the antibody; a method for detecting the expression
CC of a B Lymphocyte Stimulator protein; a method for diagnosing an
CC autoimmune disease or a B cell cancer; and a method for treating,
CC preventing, or ameliorating an autoimmune disease or a B cell cancer. The
CC antibody is useful for detecting expression of B Lymphocyte Stimulator
CC protein, and in diagnosing, treating, preventing, or ameliorating an
CC autoimmune disease or a B cell cancer. The autoimmune disease is systemic
CC lupus erythematosus or Rheumatoid arthritis. It can also be used for
CC diagnosing, treating, and preventing immune disorders (e.g. multiple
CC sclerosis, myasthenia gravis, or Hashimoto's disease), inflammatory
CC disorders (e.g. asthma or allergic disorders), infectious diseases (e.g.
CC AIDS), and proliferative disorders (e.g. leukemia, carcinoma, or
CC lymphoma). This sequence represents the heavy chain variable
CC complementary determining region 3 of a single-chain variable fragment
CC polypeptide that immunospecifically binds to a B Lymphocyte Stimulator
CC protein of the invention. Note: This sequence is not shown in the
CC specification. It has been electronically downloaded from the USPTO
CC website.

XX Sequence 14 AA;

Query Match 37.5%; Score 36; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 FPOHGL 15
Db 7 FPOHGL 12

RESULT 6

ID AEE33637 standard; peptide; 16 AA.

XX AEE33637;

DT 09-FEB-2006 (first entry)

DE Wheat gliadin/glutein epitope SEQ ID NO 323.

XX Immunosuppressive; Gastrointestinal-Gen.; T-cell-receptor-agonist;
KM T-cell-receptor-antagonist; Vaccine; celiac disease; immunogenicity;
KW gastrointestinal disease; immune disorder; gluten protein; gliadin.

XX Triticum aestivum.

PN WO2005105129-A2.

PD 10-NOV-2005.

PF 28-APR-2005; 2005WO-GB001621.

PR 28-APR-2004; 2004AU-00201774.

PR 11-FEB-2005; 2005AU-00900650.

XX (BTGT-) BTG INT LTD.

PI Anderson R, Beisbach T, Din JT;

DR WPI; 2005-769484/78.

PT Preventing or treating celiac disease comprises administering to an
PT individual a peptide (analogue) comprising at least one T cell epitope
PT (e.g. a wheat and/or an oat epitope).

PS Claim 1; SEQ ID NO 323; 94pp; English.

CC The invention relates to a method of preventing or treating celiac
CC disease comprises administering to an individual at least one agent
CC selected from a peptide comprising at least one epitope, given in the
CC specification, or their equivalents, and an analogue of the peptide,

CC which is capable of being recognized by a T cell receptor that recognizes
CC the peptide. The methods, agents, antagonists and compositions are useful
CC for treating or preventing celiac disease. The agent or antagonist, or
CC wild type sequence is useful for producing an antibody specific to the
CC agent, antagonist or wild type sequence. The mutation in an epitope of a
CC gluten protein is useful for decreasing the ability of the gluten protein
CC to cause celiac disease. The present sequence represents the amino acid
CC sequence of a wheat gliadin/glutein epitope.

XX Sequence 16 AA;

Query Match 36.5%; Score 35; DB 9; Length 16;
Best Local Similarity 54.5%; Pred. No. 1.8e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 4 QKVDQFPQHG 14
Db 6 QQPEQDFPQFG 16

RESULT 7

ID AEE34193 standard; peptide; 16 AA.

XX AEE34193;

DT 09-FEB-2006 (first entry)

DE Wheat gliadin/glutein epitope SEQ ID NO 879.

XX Immunosuppressive; Gastrointestinal-Gen.; T-cell-receptor-agonist;
KM T-cell-receptor-antagonist; Vaccine; celiac disease; immunogenicity;
KW gastrointestinal disease; immune disorder; gluten protein; gliadin.

XX Triticum aestivum.

PN WO2005105129-A2.

PD 10-NOV-2005.

PF 28-APR-2005; 2005WO-GB001621.

PR 28-APR-2004; 2004AU-00201774.

PR 11-FEB-2005; 2005AU-00900650.

XX (BTGT-) BTG INT LTD.

PI Anderson R, Beisbach T, Din JT;

DR WPI; 2005-769484/78.

PT Preventing or treating celiac disease comprises administering to an
PT individual a peptide (analogue) comprising at least one T cell epitope
PT (e.g. a wheat and/or an oat epitope).

PS Claim 1; SEQ ID NO 879; 94pp; English.

CC The invention relates to a method of preventing or treating celiac
CC disease comprises administering to an individual at least one agent
CC selected from a peptide comprising at least one epitope, given in the
CC specification, or their equivalents, and an analogue of the peptide,
CC which is capable of being recognized by a T cell receptor that recognizes
CC the peptide. The methods, agents, antagonists and compositions are useful
CC for treating or preventing celiac disease. The agent or antagonist, or
CC wild type sequence is useful for producing an antibody specific to the
CC agent, antagonist or wild type sequence. The mutation in an epitope of a
CC gluten protein is useful for decreasing the ability of the gluten protein
CC to cause celiac disease. The present sequence represents the amino acid
CC sequence of a wheat gliadin/glutein epitope.

XX Sequence 16 AA;

Query Match 36.5%; Score 35; DB 9; Length 16;

Best Local Similarity 54.5%; Pred. No. 1.8e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 QKVDQFPQHG 14
|:|:|:|:|:|:|
Db 6 QKPEQGFQPG 16

RESULT 8

ADRI0610
ID ADRI0610 standard; peptide: 18 AA.

AC ADRI0610;

DT 21-OCT-2004 (first entry)

DE Cat IGE epitope recognised by monoclonal antibody 3.76, SEQ ID 10.

KM Antiaesthetic; Antiallergic; Immunosuppressive; IGE; dog; asthma;

KM anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;

OS Felis catus.

PN W02004065936-A2.

PD 05-AUG-2004.

PF 15-JAN-2004; 2004WO-US003566.

PR 16-JAN-2003; 2003US-0440472P.

PA (UYNC-) UNIV NORTH CAROLINA STATE.

PI Hammerberg B;

DR WPI; 2004-593545/57.

PT Novel antibody that specifically binds to mammalian IGE epitope, useful

PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE

PT or treating asthma or anaphylactic shock.

PS Example 6; Page 9; 14pp; English.

CC The present invention relates to a novel monoclonal antibody (1) that

CC specifically binds to a mammalian IGE epitope, where the epitope is

CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.

CC (1) is useful for testing an allergen reactivity of an IGE sample. The

CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut

CC and corn allergens. The sample is a biological sample collected from a

CC dog, cat or horse. (1) is also useful for detecting mammalian IGE and for

CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal

CC antibodies recognise epitopes on canine IGE corresponding to amino acid

CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the

CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from

CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and

CC 3.76 were observed to have good cross-reactivity with the epsilon-chain

CC of IGE from cat and horse, but did not exhibit cross-reactivity with

CC either pig or human epsilon-chains of IGE. The present sequence is the

CC cat IGE 3.76 recognition site.

XX Sequence 18 AA;

XX Query Match 36.5%; Score 35; DB 8; Length 18;

XX Best Local Similarity 44.4%; Pred. No. 2e+02;

XX Matches 8; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 IDGQKVDQFPQHG 18
|:|:|:|:|:|:|
Db 1 VDGQKATIRFPYTA PGKQ 18

RESULT 9

AAR50232
ID AAR50232 standard; protein: 15 AA.

AC AAR50232;

DT 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 09-OCT-1994 (first entry)

DE Sequence of NH2 terminal fragment of Group A streptococcal surface

DE protein M3.

OS Streptococcus sp.

PN W09406465-A1.

PD 31-MAR-1994.

PF 15-SEP-1993; 93WO-US008704.

PR 16-SEP-1992; 92US-00945860.

PA (UYTE-) UNIV TENNESSEE RES CORP.

PI Dale JB;

DR WPI; 1994-118162/14.

PT New recombinant hybrid streptococcal M protein antigen(s) - which elicit

PT opsonic antibodies without eliciting cross-reactive antibodies to

PT mammalian heart tissue.

PS Disclosure; Page 11; 45pp; English.

CC The surface M protein of Group A streptococci is the major virulence

CC factor and protective antigen of these organisms. However, there are a

CC tremendous number of M protein serotypes. The invention provides

CC recombinant M protein antigen comprising a gene encoding a carrier

CC protein and an NH2 or COOH terminal M protein fragment carrying one or

CC more epitopes. AAR50232 is a suitable NH2-terminal fragment of M3 protein

CC for constructing antigens which elicit opsonic antibodies in an immunised

CC animal when linked or fused to an appropriate carrier. (Updated on 25-

CC MAR-2003 to correct PN field.) (Updated on 27-AUG-2003 to correct OS

CC field.)

XX Sequence 15 AA;

XX Query Match 35.4%; Score 34; DB 2; Length 15;

XX Best Local Similarity 41.7%; Pred. No. 2.4e+02;

XX Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 DGQKVDQFPQHG 13
|:|:|:|:|:|:|
Db 1 DARSVNGEFPFH 12

RESULT 10

ABP94693
ID ABP94693 standard; peptide: 15 AA.

AC ABP94693;

DT 28-MAR-2003 (first entry)

DE HLA protein 121P2A3 peptide #11048.

DE Human, 121P2A3; cytostatic; immunostimulant; vaccine; SSH;

KW humoral immune response; cellular immune response;

KW suppression subtractive hybridisation; HLA; human leukocyte antigen.

OS	Homo sapiens.
XX	
PN	WO200283068-A2.
XX	
PD	24-OCT-2002.
XX	
PF	09-APR-2002; 2002MO-US011359.
XX	
PR	10-APR-2001; 2001US-0282739P.
XX	
PR	25-APR-2001; 2001US-0286630P.
XX	
XX	22-JUN-2001; 2001US-0300373P.
XX	
PA	(AGEN-) AGENSYS INC.
XX	
PI	Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC,
XX	
PI	Afar DEH, Safiran D, Morrison K, Morrison RK, Ge W, Jakobovits A,
XX	
DR	WPI; 2003-092956/08.
XX	
PT	New composition comprising a substance that modulates the status of
XX	
PT	121P2A3 polypeptides, useful for eliciting humoral or cellular immune
XX	
PT	responses or in assessing the status of 121P2A3 gene products in normal
XX	
PT	versus cancerous tissues.
XX	
PS	Claim 13; Page 270; 362pp; English.
XX	
CC	The invention relates to a novel composition comprising a substance that
XX	
CC	modulates the status of a protein, 121P2A3. The composition of the
XX	
CC	invention has cytostatic and immunostimulant activity, and is useful as a
XX	
CC	vaccine. The 121P2A3 proteins and polynucleotides are useful for
XX	
CC	eliciting humoral or cellular immune response. The polynucleotides are
XX	
CC	useful for characterizing cytogenetic abnormalities of this chromosomal
XX	
CC	locus, as tools that can be used to delineate cytogenetic abnormalities
XX	
CC	in the chromosomal region that encodes 121P2A3 that may contribute to
XX	
CC	malignant phenotype, and in assessing the status of 121P2A3 gene products
XX	
CC	in normal versus cancerous tissues. The proteins are useful for
XX	
CC	generating and characterizing domain-specific antibodies, for identifying
XX	
CC	agents or cellular factors that bind to 121P2A3 or a particular structure
XX	
CC	domain, and in various therapeutic and diagnostic contexts, including
XX	
CC	cancer vaccines. The antibodies or T cells reactive with the product are
XX	
CC	useful in passive or active immunisation, and in imaging methodologies
XX	
CC	for the management of cancer. The sequences shown in ABP93646 - ABP95595
XX	
CC	represent peptides from the 121P2A3 variants of the invention
XX	
SQ	Sequence 15 AA;
XX	
Query Match	35.4%; Score 34; DB 6; Length 15;
Best Local Similarity	40.0%; Pred No. 2.4e+02;
Matches	6; Conservative 4; Mismatches 5; Indels 0; Gaps 0.
Oy	2 DQQKVDQEPQHGVL 16
	: : : : : :
Db	1 ENEKLDROHVQHQL 15
RESULT 11	
ABP95588	
ID	ABP95588 standard; peptide; 15 AA.
XX	
AC	ABP95588;
XX	
DT	28-MAR-2003 (first entry)
XX	
DE	HLA protein 121P2A3 peptide #11943.
XX	
XX	
KW	Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
XX	
KW	humoral immune response; cellular immune response;
XX	
KW	suppression subtractive hybridisation; HLA; human leukocyte antigen.
OS	Homo sapiens.
XX	
XX	
PN	WO200283068-A2.
XX	

PD	24-OCT-2002.
XX	
PF	09-APR-2002; 2002WO-US011359.
XX	
PR	10-APR-2001; 2001US-0282739P.
PR	25-APR-2001; 2001US-0286630P.
PR	22-JUN-2001; 2001US-0300373P.
XX	
PA	(AGEN-) AGENSYS INC.
PI	Challita-Eid PM, Raitano AB, Paris M, Hubert RS, Mitchell SC;
PI	Afar DBH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
DR	WPI; 2003-092956/08.
XX	
PT	New composition comprising a substance that modulates the status of
PT	121P2A3 polypeptides, useful for eliciting humoral or cellular immune
PT	responses or in assessing the status of 121P2A3 gene products in normal
XX	versus cancerous tissues.
XX	
PS	Claim 13; Page 287; 362pp; English.
XX	
CC	The invention relates to a novel composition comprising a substance that
CC	modulates the status of a protein, 121P2A3. The composition of the
CC	invention has cyostatic and immunostimulant activity, and is useful as a
CC	vaccine. The 121P2A3 proteins and polynucleotides are useful for
CC	eliciting humoral or cellular immune response. The polynucleotides are
CC	useful for characterising cytogenetic abnormalities of this chromosomal
CC	locus, as tools that can be used to delineate cytogenetic abnormalities
CC	in the chromosomal region that encodes 121P2A3 that may contribute to
CC	malignant phenotype, and in assessing the status of 121P2A3 gene products
CC	in normal versus cancerous tissues. The proteins are useful for
CC	generating and characterising domain-specific antibodies, for identifying
CC	agents or cellular factors that bind to 121P2A3 or a particular structure
CC	domain, and in various therapeutic and diagnostic contexts, including
CC	cancer vaccines. The antibodies or T cells reactive with the product are
CC	useful in passive or active immunisation, and in imaging methodologies
CC	for the management of cancer. The sequences shown in ABP83646 - ABP95595
XX	represent peptides from the 121P2A3 variants of the invention
XX	
SO	Sequence 15 AA;
	Query Match 35.4%; Score 34; DB 6; Length 15;
	Best Local Similarity 40.0%; Pred. No. 2.4e+02;
	Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY	2 DGQKVDSEFPQGLV 16
	: : : : :
Db	1 ENKKLDROHVQHLL 15
RESULT 12	
ID	ABP95194
XX	ABP95194; standard; peptide; 15 AA.
AC	
XX	ABP95194;
DT	28-MAR-2003 (first entry)
XX	
DE	HLA protein 121P2A3 peptide #11549.
XX	
KM	Human; 121P2A3; cytostatic; immunostimulant; vaccine; SSH;
KM	humoral immune response; cellular immune response;
XX	suppression subreactive hybridisation; HLA; human leukocyte antigen.
XX	
OS	Homo sapiens.
XX	
PN	WO200283068-A2.
XX	
PD	24-OCT-2002.
XX	
PF	09-APR-2002; 2002WO-US011359.
XX	

PR 10-APR-2001; 2001US-0282739P.
 PR 25-APR-2001; 2001US-0286630P.
 PR 22-JUN-2001; 2001US-0300373P.
 XX
 PA (AGEN-) AGENSYS INC.
 PI Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Mitchell SC;
 PI Alar DEH, Saffran D, Morrison K, Morrison RK, Ge W, Jakobovits A;
 XX WPI; 2003-092956/08.
 XX
 PT New composition comprising a substance that modulates the status of
 PT 121P2A3 polypeptides, useful for eliciting humoral or cellular immune
 PT responses or in assessing the status of 121P2A3 gene products in normal
 PT versus cancerous tissues.
 XX
 PS Claim 13; Page 279; 362pp; English.
 XX
 CC The invention relates to a novel composition comprising a substance that
 CC modulates the status of a protein, 121P2A3. The composition of the
 CC invention has cytoskeletal and immunostimulant activity, and is useful as a
 CC vaccine. The 121P2A3 proteins and polynucleotides are useful for
 CC eliciting humoral or cellular immune response. The polynucleotides are
 CC useful for characterizing cytogenetic abnormalities of this chromosomal
 CC locus, as tools that can be used to delineate cytogenetic abnormalities
 CC in the chromosomal region that encodes 121P2A3 that may contribute to
 CC malignant phenotype, and in assessing the status of 121P2A3 gene products
 CC in normal versus cancerous tissues. The proteins are useful for
 CC generating and characterizing domain-specific antibodies, for identifying
 CC agents or cellular factors that bind to 121P2A3 or a particular structure
 CC domain, and in various therapeutic and diagnostic contexts, including
 CC cancer vaccines. The antibodies or T cells reactive with the product are
 CC useful in passive or active immunisation, and in imaging methodologies
 CC for the management of cancer. The sequences shown in ABP83646 - ABP95595
 CC represent peptides from the 121P2A3 variants of the invention
 XX
 SQ Sequence 15 AA;
 Qy Query Match 35.4%; Score 34; DB 6; Length 15;
 Db Best Local Similarity 40.0%; Pred. No. 2.4e+02;
 Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
 Qy 2 DGQKVDQFPQHGIV 16
 Db 1 ENKLDROHVQHLL 15
 RESULT 13
 ADM96833
 ID ADM96833 standard; peptide; 17 AA.
 XX
 AC ADM96833;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Tissue factor VIIA (TFVIIA) peptide antagonist #249.
 XX
 KW tissue factor VIIa; TFVIIa; chronic thromboembolic disease;
 KW fibrin formation; vascular disorders; deep venous thrombosis;
 KW arterial thrombosis; stroke; atherosclerosis; septicemia.
 XX
 OS Synthetic.
 XX
 PN US2004087767-A1.
 XX
 PD 06-MAY-2004.
 XX
 PF 30-JAN-2003; 2003US-00356257.
 XX
 PR 06-FEB-2002; 2002US-0355420P.
 XX
 PA (GETH) GENENTECH INC.
 XX

PI Lazarus RA, Maun HR;
 XX WPI; 2004-356247/33.
 DR
 XX
 PT New peptide, useful for preventing or treating chronic thromboembolic
 PT diseases or disorders associated with fibrin formation including vascular
 PT disorders, such as deep venous thrombosis, arterial thrombosis, and
 PT stroke.
 XX
 PS Example 2; SEQ ID NO 255; 102pp; English.
 XX
 CC The invention relates to peptide antagonists of tissue factor VIIa
 CC (TFVIIa) and a method of inhibiting FVIIa activity by contacting FVIIa
 CC with the peptide in the presence of tissue factor and under conditions
 CC that allow binding of the compound to FVIIa to occur. The peptides are
 CC useful for preventing or treating chronic thromboembolic diseases or
 CC disorders associated with fibrin formation including vascular disorders,
 CC such as deep venous thrombosis, arterial thrombosis, stroke,
 CC atherosclerosis, or septicemia. The present sequence represents a TFVIIa
 CC peptide antagonist of the invention.
 XX
 SQ Sequence 17 AA;
 Qy Query Match 35.4%; Score 34; DB 8; Length 17;
 Db Best Local Similarity 50.0%; Pred. No. 2.7e+02;
 Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 Qy 3 GQKVDQFPQ 12
 Db 1 GEGVEEFPPE 10
 RESULT 14
 ADR10609
 ID ADR10609 standard; peptide; 18 AA.
 XX
 AC ADR10609;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Dog IgE epitope recognised by monoclonal antibody 3.76, SEQ ID 9.
 XX
 KW Antihaematic; Antiallergic; Immunosuppressive; IgE; dog; asthma;
 KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody.
 XX
 OS Canis familiaris.
 XX
 PN WO2004065936-A2.
 XX
 PD 05-AUG-2004.
 XX
 PF 15-JAN-2004; 2004WO-US003566.
 XX
 PR 16-JAN-2003; 2003US-0440472P.
 XX
 PA (UNNC-) UNIV NORTH CAROLINA STATE.
 XX
 PI Hammerberg B;
 XX
 DR WPI; 2004-593545/57.
 XX
 PT Novel antibody that specifically binds to mammalian IgE epitope, useful
 PT for testing an allergen reactivity of IgE sample, detecting mammalian IgE
 PT or treating asthma or anaphylactic shock.
 XX
 PS Example 6; Page 9; 14pp; English.
 XX
 CC The present invention relates to a novel monoclonal antibody (I) that
 CC specifically binds to a mammalian IgE epitope, where the epitope is
 CC between amino acids 145-166 or 356-374 of mammalian IgE, e.g. dog IgE.
 CC (I) is useful for testing an allergen reactivity of an IgE sample. The
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
 CC and corn allergens. The sample is a biological sample collected from a

CC dog, cat or horse. (1) is also useful for detecting mammalian IgE and for
CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
CC antibodies recognise epitopes on canine IgE corresponding to amino acid
CC residues 357-371 (ADR1601) and 146-162 (ADR1009) respectively of the
CC canine IgE epsilon-chain. Recognition of epsilon-chains from IgE from
CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
CC of IgE from cat and horse, but did not exhibit cross-reactivity with
CC either pig or human epsilon-chains of IgE.

XX
SQ Sequence 18 AA;

Query Match 35.4%; Score 34; DB 8; Length 18;

Best Local Similarity 54.5%; Pred. No. 2.9e+02;

Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 IDGQVDEQFP 11
:|||||
1 VDGQKATNIFP 11

RESULT 15

ADL98126
ID ADL98126 standard; peptide; 10 AA.

AC ADL98126;

DT 17-JUN-2004 (first entry)

DE Candida kefyr enone reductase peptide SEQ ID NO:9.

XX enone reductase; enzyme; levodione; ketoisophorone; carotenoid;

KM Candida kefyr; Kluyveromyces marxianus.

XX Kluyveromyces marxianus.

PN WO2004027065-A2.

XX 01-APR-2004.

XX 19-SEP-2003; 2003WO-EP010473.

XX 23-SEP-2002; 2002EP-00021098.

XX (STAM) DSM IP ASSETS BV.

XX Katakoka M, Shimizu S;

XX WPI; 2004-295422/27.

XX
PT New enone reductase, useful in improving the production process of
PT levodione, which is important in the synthesis of optically active
PT carotenoids.

XX Example 1; SEQ ID NO 9; 31pp; English.

XX
CC The present invention describes an isolated DNA (I) comprising a
CC nucleotide sequence coding for an enzyme having enone reductase activity.
CC Also described: (1) a vector or a plasmid comprising (I); (2) a host cell
CC transformed or transfected by (1) or the vector or the plasmid of (1);
CC (3) a polypeptide encoded by (1); and (4) a process for the production of
CC levodione which comprises contacting ketoisophorone with the polypeptide
CC of (3) or with the host cell of (2) or a cell-free extract under
CC conditions for the production of levodione, e.g. at pH 4.0-9.0 and at a
CC temperature of 10-60 degrees Celsius for 5 minutes to 72 hours or at pH
CC 5.0-8.0 and at a temperature of 20-60 degrees Celsius for 15 minutes to
CC 48 hours. The DNA (I) and the encoded polypeptide can be used in
CC improving the production process of levodione, which is important in the
CC synthesis of optically active carotenoids. The present sequence
CC represents a Candida kefyr (Kluyveromyces marxianus) enone reductase
CC peptide, which is used in the exemplification of the present invention.
XX
SQ Sequence 10 AA;

Query Match 34.4%; Score 33; DB 8; Length 10;
Best Local Similarity 71.4%; Pred. No. 2.2e+02;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 11 PQHGLVK 17
:|||||
DB 4 PQHGIRK 10

Search completed: May 30, 2006, 15:04:05
Job time : 63.6667 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 30, 2006, 15:17:23 ; Search time 49.3333 Seconds
(without alignments)
169.011 Million cell updates/sec

Title: US-10-758-165A-11

Sequence: 1 IDGQKVDQEPFGHGLVQK 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 432914

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:*

- 1: /EMC_Celerra_sids3/prodata/2/pubppa/us07_PUBCOMB.pep:*
- 2: /EMC_Celerra_sids3/prodata/2/pubppa/us08_PUBCOMB.pep:*
- 3: /EMC_Celerra_sids3/prodata/2/pubppa/us09_PUBCOMB.pep:*
- 4: /EMC_Celerra_sids3/prodata/2/pubppa/us10_PUBCOMB.pep:*
- 5: /EMC_Celerra_sids3/prodata/2/pubppa/us10B_PUBCOMB.pep:*
- 6: /EMC_Celerra_sids3/prodata/2/pubppa/us11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	18	5	US-10-758-165-11
2	78	81.2	15	4	US-10-052-788-5
3	36	37.5	14	3	US-09-880-748-2449
4	36	37.5	14	4	US-10-293-418-2449
5	36	37.5	14	6	US-11-054-515-2449
6	36	37.5	14	6	US-11-266-444-2449
7	35	36.5	15	4	US-10-758-165-10
8	34	35.4	15	4	US-10-141-627-11
9	34	35.4	17	4	US-10-356-257-255
10	34	35.4	18	5	US-10-758-165-9
11	33	34.4	13	6	US-11-127-804-9
12	32	33.3	10	4	US-10-079-709-3
13	32	33.3	10	6	US-11-036-272-3
14	32	33.3	14	3	US-09-880-748-2446
15	32	33.3	14	3	US-09-880-748-2703
16	32	33.3	14	4	US-10-293-418-2446
17	32	33.3	14	4	US-10-293-418-2703
18	32	33.3	14	5	US-10-865-478-842
19	32	33.3	14	6	US-11-054-515-2446
20	32	33.3	14	6	US-11-054-515-2703
21	32	33.3	14	6	US-11-266-444-2446
22	32	33.3	14	6	US-11-266-444-2703
23	31	32.3	14	3	US-09-880-748-2146
24	31	32.3	14	3	US-09-880-748-2151
25	31	32.3	14	4	US-10-293-418-2146
26	31	32.3	14	4	US-10-293-418-2151
27	31	32.3	14	6	US-11-054-515-2146

28	31	32.3	14	6	US-11-054-915-2151	Sequence 2151, Ap
29	31	32.3	14	6	US-11-266-444-2146	Sequence 2146, Ap
30	31	32.3	14	6	US-11-266-444-2151	Sequence 2151, Ap
31	31	32.3	15	4	US-10-059-261-108	Sequence 108, App
32	31	32.3	15	4	US-10-059-261-216	Sequence 216, App
33	31	32.3	15	5	US-10-627-649-108	Sequence 108, App
34	31	32.3	15	5	US-10-627-649-216	Sequence 216, App
35	31	32.3	18	5	US-10-758-165-15	Sequence 15, Appl
36	30	31.2	10	4	US-10-353-929-166	Sequence 166, App
37	30	31.2	11	3	US-09-977-827-8	Sequence 8, Appl1
38	30	31.2	17	3	US-09-864-761-46580	Sequence 46580, A
39	29.5	30.7	17	4	US-10-356-257-114	Sequence 114, App
40	29	30.2	11	3	US-09-977-827-13	Sequence 13, Appl
41	29	30.2	12	5	US-10-500-878-14	Sequence 14, Appl
42	29	30.2	13	6	US-11-152-974A-272	Sequence 272, App
43	29	30.2	13	6	US-11-153-143A-272	Sequence 272, App
44	29	30.2	14	5	US-10-476-362-26	Sequence 26, Appl
45	29	30.2	15	4	US-10-282-960-23	Sequence 23, Appl

ALIGNMENTS

```
RESULT 1
US-10-758-165-11
Sequence 11, Application US/10758165
Publication No. US20050196816A1
GENERAL INFORMATION:
APPLICANT: Hammeberg, Bruce
TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
FILE REFERENCE: 5051-661
CURRENT APPLICATION NUMBER: US/10/758,165
CURRENT FILING DATE: 2004-01-16
PRIOR APPLICATION NUMBER: US 60/440,472
PRIOR FILING DATE: 2003-01-16
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.2
SEQ ID NO 11
LENGTH: 18
TYPE: PRT
ORGANISM: Equus caballus
US-10-758-165-11

Query Match      100.0%; Score 96; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. NO. 9.4e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1 IDGQKVDQEPFGHGLVQK 18
Db      1 IDGQKVDQEPFGHGLVQK 18

RESULT 2
US-10-052-788-5
Sequence 5, Application US/10052788
Publication No. US20030087314A1
GENERAL INFORMATION:
APPLICANT: Gershwin, Laurel J.
APPLICANT: Pettigrew, Howard David
APPLICANT: Kalina, Warren V.
TITLE OF INVENTION: Bpelson Immunoglobulin Chain Derived Peptides for
FILE REFERENCE: 023070-121000US
CURRENT APPLICATION NUMBER: US/10/052,788
CURRENT FILING DATE: 2001-11-08
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
```

OTHER INFORMATION: Description of Artificial Sequence:epitope peptide
OTHER INFORMATION: PS, middle portion of C2 of equine IGE epsilon
OTHER INFORMATION: heavy chain
US-10-052-788-5

Query Match 81.2%; Score 78; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 7,4e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 IDGQKVDQFPQHG 14
Db 2 IDGQKVDQFPQHG 15

RESULT 3

US-09-880-748-2449
Sequence 2449, Application US/09880748
Publication No. US2003005937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PFS23
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2449
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-2449

Query Match 37.5%; Score 36; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 FPOHGL 15
Db 7 FPOHGL 12

RESULT 4

US-10-293-418-2449
Sequence 2449, Application US/10293418
Publication No. US2003022396A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PFS23P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16

PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 2449
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-2449

Query Match 37.5%; Score 36; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 FPOHGL 15
Db 7 FPOHGL 12

RESULT 5

US-11-054-515-2449
Sequence 2449, Application US/11054515
Publication No. US20050255532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PFS23P3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 2449
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-2449

Query Match 37.5%; Score 36; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 FPOHGL 15
Db 7 FPOHGL 12

RESULT 6

US-11-266-444-2449
Sequence 2449, Application US/11266444
Publication No. US20060052789A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.

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; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to B Lymphocyte Stimulac
; FILE REFERENCE: PFS2P1D1
; CURRENT APPLICATION NUMBER: US/11/266,444
; CURRENT FILING DATE: 2005-11-04
; PRIOR APPLICATION NUMBER: 09/880,746
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2449
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-266-444-2449

Query Match      37.5%; Score 36; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 63;
Matches      6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      10 FPOHGL 15
      |||||
Db      7 FPOHGL 12

RESULT 7
US-10-758-165-10
; Sequence 10, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Felis catus
; US-10-758-165-10

Query Match      36.5%; Score 35; DB 5; Length 18;
Best Local Similarity 44.4%; Pred. No. 1.2e+02;
Matches      8; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy      1 IDGQVDEQFPQHGVLVXQ 18
      :|||:
Db      1 VDGQKATNIFPYTAPGKQ 18

RESULT 8
US-10-141-627-11
; Sequence 11, Application US/10141627
; Publication No. US2002017663A1
; GENERAL INFORMATION:
; APPLICANT: Dale, James B.
; TITLE OF INVENTION: ANTIGEN OF HYBRID M PROTEIN AND CARRIER
; FILE REFERENCE: 48112.404C3
; CURRENT APPLICATION NUMBER: US/10/141,627
; CURRENT FILING DATE: 2002-05-07
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; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: NH2-terminal fragment of M protein for
; OTHER INFORMATION: constructing antigen, which elicit opsonic
; US-10-141-627-11

Query Match      35.4%; Score 34; DB 4; Length 15;
Best Local Similarity 41.7%; Pred. No. 1.5e+02;
Matches      5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy      2 DGQVDEQFPQH 13
      |::|:
Db      1 DARSVNGEPRH 12

RESULT 9
US-10-356-257-255
; Sequence 255, Application US/10356257
; Publication No. US20040087767A1
; GENERAL INFORMATION:
; APPLICANT: LAZARUS, ROBERT A.
; APPLICANT: MAUN, HENRY R.
; TITLE OF INVENTION: Fv1a Antagonists
; FILE REFERENCE: P1950R1
; CURRENT APPLICATION NUMBER: US/10/356,257
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/355,420
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 355
; SEQ ID NO 255
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
; US-10-356-257-255

Query Match      35.4%; Score 34; DB 4; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches      5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy      3 GQKYDEQFPQ 12
      |::|:
Db      1 GEQVEERPE 10

RESULT 10
US-10-758-165-9
; Sequence 9, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Canis familiaris
; US-10-758-165-9

Query Match      35.4%; Score 34; DB 5; Length 18;
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Best Local Similarity 54.5%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Oy 1 IDGQKVDQFP 11
: ||| :
Db 1 VDGQKATNIFP 11

RESULT 11

US-11-127-804-9
; Sequence 9, Application US/11127804
; Publication No. US2006003940A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Rong-Hwa
; TITLE OF INVENTION: T-CELL DEATH-INDUCING EPITOPES
; FILE REFERENCE: 113062-009001
; CURRENT APPLICATION NUMBER: US/11/127,804
; CURRENT FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,161
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-11-127-804-9

Query Match 34.4%; Score 33; DB 6; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.8e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy 3 GQKVDQFPQHG 14
: ||| :
Db 2 GQKVDQFPWPHSG 13

RESULT 12

US-10-079-709-3
; Sequence 3, Application US/10079709
; Publication No. US20030119163A1
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Selen
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phylase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/079,709
; FILING DATE: 02-FEB-2002
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/233,510

FILING DATE: 20-JAN-1999
APPLICATION NUMBER: 07/688,578
FILING DATE: 24-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24615-20026.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-327-7250
TELEFAX: 415-327-2951

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
FRAGMENT TYPE: N-terminal
US-10-079-709-3

Query Match 33.3%; Score 32; DB 4; Length 10;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 6 VDEQFPQHG 14
: ||| :
Db 2 VDERFPYTG 10

RESULT 13

US-11-036-272-3
; Sequence 3, Application US/11036272
; Publication No. US20060063243A1
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Selen
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phylase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/036,272
; FILING DATE: 14-JAN-2005
; CLASSIFICATION:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/036,272
; FILING DATE: 20-JAN-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/688,578
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24615-20026.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-327-7250
TELEFAX: 415-327-2951

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; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 10 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   HYPOTHEICAL: NO
;   FRAGMENT TYPE: N-terminal
US-11-036-272-3
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Query Match          33.3%; Score 32; DB 6; Length 10;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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```
QY      6 VDEQFPQHG 14
        |||:|
Db       2 VDERFPYTG 10
```

```
RESULT 14
US-09-880-748-2446
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```
; Sequence 2446, Application US/09880748
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```
; Publication No. US2003005937A1
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: Ruben et al.
```

```
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
```

```
; FILE REFERENCE: PF523
```

```
; CURRENT APPLICATION NUMBER: US/09/880,748
```

```
; CURRENT FILING DATE: 2001-06-15
```

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; PRIOR APPLICATION NUMBER: 60/212,210
```

```
; PRIOR FILING DATE: 2000-06-15
```

```
; PRIOR APPLICATION NUMBER: 60/240,816
```

```
; PRIOR FILING DATE: 2000-10-17
```

```
; PRIOR APPLICATION NUMBER: 60/276,248
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; PRIOR FILING DATE: 2001-03-16
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; PRIOR APPLICATION NUMBER: 60/277,379
```

```
; PRIOR FILING DATE: 2001-03-21
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```
; PRIOR APPLICATION NUMBER: 60/293,499
```

```
; PRIOR FILING DATE: 2001-05-25
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; NUMBER OF SEQ ID NOS: 3239
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; SOFTWARE: Patentln Ver. 2.0
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; SEQ ID NO 2446
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; LENGTH: 14
```

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; TYPE: PRT
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; ORGANISM: Homo sapiens
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US-09-880-748-2446
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Query Match          33.3%; Score 32; DB 3; Length 14;
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Best Local Similarity 100.0%; Pred. No. 2.9e+02;
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      10 FPQHG 14
        |||
Db       7 FPQHG 11
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RESULT 15
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US-09-880-748-2703
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; Sequence 2703, Application US/09880748
```

```
; Publication No. US2003005937A1
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```
; GENERAL INFORMATION:
```

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; APPLICANT: Ruben et al.
```

```
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
```

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; FILE REFERENCE: PF523
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; CURRENT APPLICATION NUMBER: US/09/880,748
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; CURRENT FILING DATE: 2001-06-15
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; PRIOR APPLICATION NUMBER: 60/212,210
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; PRIOR FILING DATE: 2000-06-15
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; PRIOR APPLICATION NUMBER: 60/240,816
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; PRIOR FILING DATE: 2000-10-17
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; PRIOR APPLICATION NUMBER: 60/276,248
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; PRIOR FILING DATE: 2001-03-16
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; PRIOR APPLICATION NUMBER: 60/277,379
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; PRIOR FILING DATE: 2001-03-21
```

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; PRIOR APPLICATION NUMBER: 60/293,499
```

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; PRIOR FILING DATE: 2001-05-25
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; NUMBER OF SEQ ID NOS: 3239
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; SOFTWARE: Patentln Ver. 2.0
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; SEQ ID NO 2703
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; LENGTH: 14
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; TYPE: PRT
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; ORGANISM: Homo sapiens
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US-09-880-748-2703
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Query Match          33.3%; Score 32; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      10 FPQHG 14
        |||
Db       7 FPQHG 11
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OM protein - protein search, using sw model

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(without alignments)
50.118 Million cell updates/sec

Title: US-10-758-165A-11
Sequence: 1 IDGQKVDQEPFQHGVLKQ 18

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Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 11137335 residues

Total number of hits satisfying chosen parameters: 11661

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:*

- 1: /EMC_Celerra_SIDS3/ptocdata/1/pubppa/US09_NEW_PUB pep:*
- 2: /EMC_Celerra_SIDS3/ptocdata/1/pubppa/US06_NEW_PUB pep:*
- 3: /EMC_Celerra_SIDS3/ptocdata/1/pubppa/US07_NEW_PUB pep:*
- 4: /EMC_Celerra_SIDS3/ptocdata/1/pubppa/US08_NEW_PUB pep:*
- 5: /EMC_Celerra_SIDS3/ptocdata/1/pubppa/PCF_NEW_PUB pep:*
- 6: /EMC_Celerra_SIDS3/ptocdata/1/pubppa/US10_NEW_PUB pep:*
- 7: /EMC_Celerra_SIDS3/ptocdata/1/pubppa/US11_NEW_PUB pep:*
- 8: /EMC_Celerra_SIDS3/ptocdata/1/pubppa/US60_NEW_PUB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	30.2	9	7	US-11-332-378-136
2	29	30.2	15	7	US-11-140-487A-2148
3	28	29.2	15	6	US-10-544-499-3
4	26	27.1	16	7	US-11-281-644A-2
5	25	26.0	10	7	US-11-122-986-795
6	25	26.0	14	7	US-11-301-554-2108
7	25	26.0	16	6	US-10-522-356-9
8	25	26.0	17	7	US-11-244-348A-7
9	24	25.0	9	7	US-11-332-378-216
10	23	24.0	9	7	US-11-140-487A-794
11	23	24.0	10	7	US-11-140-487A-795
12	23	24.0	10	7	US-11-140-487A-1029
13	23	24.0	14	7	US-11-122-986-542
14	22	22.9	9	7	US-11-122-986-789
15	22	22.9	11	7	US-11-122-986-673
16	22	22.9	15	6	US-10-490-949-35
17	22	22.9	15	6	US-10-543-587-10
18	22	22.9	17	7	US-11-297-317-23
19	22	22.9	18	7	US-11-213-668-90
20	21	21.9	10	6	US-10-538-066-557
21	21	21.9	10	6	US-11-140-487A-990
22	21	21.9	11	6	US-10-538-066-588
23	21	21.9	12	1	US-09-784-950-9
24	21	21.9	13	6	US-10-538-066-589
25	21	21.9	14	7	US-11-219-563-38

26	21	21.9	15	7	US-11-118-324-4	Sequence 4, Appli
27	21	21.9	17	7	US-11-122-086-398	Sequence 398, App
28	20	20.8	7	7	US-11-122-086-669	Sequence 669, App
29	20	20.8	8	6	US-10-546-594-38	Sequence 38, Appl
30	20	20.8	9	6	US-10-538-066-326	Sequence 326, App
31	20	20.8	9	6	US-10-538-066-346	Sequence 346, App
32	20	20.8	9	7	US-11-054-072-89	Sequence 89, Appl
33	20	20.8	9	7	US-11-140-487A-1608	Sequence 1608, Ap
34	20	20.8	9	7	US-11-167-773-83	Sequence 83, Appl
35	20	20.8	9	7	US-11-332-378-59	Sequence 59, Appl
36	20	20.8	9	7	US-11-332-378-63	Sequence 63, Appl
37	20	20.8	10	6	US-10-538-066-131	Sequence 131, App
38	20	20.8	10	6	US-10-538-066-132	Sequence 132, App
39	20	20.8	10	6	US-10-538-066-328	Sequence 328, App
40	20	20.8	10	6	US-10-538-066-348	Sequence 348, App
41	20	20.8	10	6	US-10-538-066-394	Sequence 394, App
42	20	20.8	10	7	US-11-219-563-16	Sequence 16, Appl
43	20	20.8	10	7	US-11-140-487A-1506	Sequence 1506, Ap
44	20	20.8	10	7	US-11-132-986-622	Sequence 622, App
45	20	20.8	10	7	US-11-332-378-60	Sequence 60, Appl

ALIGNMENTS

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RESULT 1
US-11-332-378-136
; Sequence 136, Application US/11332378
; Publication No. US20060106196A1
; GENERAL INFORMATION:
; APPLICANT: Gaudernack, Gustav
; APPLICANT: Eriksen, Jon Amund
; APPLICANT: Moller, Mona
; APPLICANT: Gjersten, Marianne Klomp
; APPLICANT: Saeterdal, Ingvald
; APPLICANT: Saebøe-Larsen, Stein
; TITLE OF INVENTION: Antigenic Peptides Derived from Telomerase
; FILE REFERENCE: 01702.401800
; CURRENT APPLICATION NUMBER: US/11/332.378
; PRIOR FILING DATE: 2006-01-17
; PRIOR APPLICATION NUMBER: US/09/743,281
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: PCT/NO99/00220
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 136
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens, other or unknown
US-11-332-378-136
Query Match 30.2%; Score 29; DB 7; Length 9;
Best Local Similarity 71.4%; Pred. No. 5.2e+04;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 QPQHG 15
Db 3 QMPAHL 9

RESULT 2
US-11-140-487A-2148
; Sequence 2148, Application US/11140487A
; Publication No. US20060093617A1
; GENERAL INFORMATION:
; APPLICANT: Immunogenetics N.V.
; TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C virus
; FILE REFERENCE: 166
; CURRENT APPLICATION NUMBER: US/11/140.487A
; PRIOR FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: EP 04012951.2
; PRIOR FILING DATE: 2004-06-01
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; PRIOR APPLICATION NUMBER: EP 04447239.7
; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: EP 05102441.2
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/576,310
; PRIOR FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: US 60/622,782
; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US 60/665,395
; PRIOR FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2278
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2148
; LENGTH: 15
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-11-140-487A-2148

Query Match 30.2%; Score 29; DB 7; Length 15;
Best Local Similarity 46.2%; Pred. No. 27;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 GQKVDQFPQHG 15
| : | | | | |
Db 1 GMDLAQEFKQKAL 13

RESULT 3
; Sequence 3, Application US/10544499
; Publication No. US20060094017A1
; GENERAL INFORMATION:
; APPLICANT: Anthony J. Conley
; APPLICANT: Beverly H. Galsinski
; APPLICANT: Allison Montalvo
; TITLE OF INVENTION: Immunogens for HIV Vaccine
; FILE REFERENCE: 21219P
; CURRENT APPLICATION NUMBER: US/10/544,499
; CURRENT FILING DATE: 2005-08-03
; PRIOR APPLICATION NUMBER: 60/447,590
; PRIOR FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: PCT/US04/05821
; PRIOR FILING DATE: 2004-02-10
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide mimotope
US-10-544-499-3

Query Match 29.2%; Score 28; DB 6; Length 15;
Best Local Similarity 50.0%; Pred. No. 40;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 9 QFPGHGLV 16
| : | | | | |
Db 2 KIPDHGIV 9

RESULT 4
US-11-281-644A-2
; Sequence 2, Application US/11281644A
; Publication No. US20060105953A1
; GENERAL INFORMATION:
; APPLICANT: Arnaud Lacoste
; APPLICANT: Christopher J. Evans
; TITLE OF INVENTION: SYSTEM FOR PROTEASE MEDIATED PROTEIN
; FILE REFERENCE: 30435.164-US-UI
; CURRENT APPLICATION NUMBER: US/11/281,644A

; CURRENT FILING DATE: 2005-11-17
; PRIOR APPLICATION NUMBER: 60/628,694
; PRIOR FILING DATE: 2004-11-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: synthetic peptide linker
US-11-281-644A-2

Query Match 27.1%; Score 26; DB 7; Length 16;
Best Local Similarity 57.1%; Pred. No. 93;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 IDGQKVD 7
| : | | |
Db 4 VDGDQVD 10

RESULT 5
US-11-122-986-795
; Sequence 795, Application US/1122986
; Publication No. US20060104989A1
; GENERAL INFORMATION:
; APPLICANT: DHARMSI, ALED
; APPLICANT: VEDADI, MASOUD
; TITLE OF INVENTION: ESSENTIAL NOVEL BACTERIAL POLYPEPTIDES
; FILE REFERENCE: IPT-330.01
; CURRENT APPLICATION NUMBER: US/11/122,986
; CURRENT FILING DATE: 2005-05-05
; PRIOR APPLICATION NUMBER: 60/423,875
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,832
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,915
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,757
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,758
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/424,367
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,376
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,370
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,362
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,373
; PRIOR FILING DATE: 2002-11-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 844
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 795
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-11-122-986-795

Query Match 26.0%; Score 25; DB 7; Length 10;
Best Local Similarity 62.5%; Pred. No. 81;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 FPGHGLVK 17
| : | | | | |
Db 3 FPEVGLKK 10

RESULT 6

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US-11-301-554-2108
; Sequence 2108, Application US/11301554
; Publication No. US20060088527A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tonglong
; APPLICANT: Matanabe, Yoshinhiro
; APPLICANT: Kaios, Michael D.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Retter, Marc W.
; APPLICANT: Durham, Margarita
; APPLICANT: Carter, Darick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedavick, Thomas S.
; APPLICANT: Bangur, Chaltanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C21
; CURRENT FILING DATE: US/11/301,554
; PRIOR APPLICATION NUMBER: US 10/283,017
; PRIOR FILING DATE: 2005-12-13
; PRIOR APPLICATION NUMBER: US 10/113,872
; PRIOR FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: US 10/113,872
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US 10/017,754
; PRIOR FILING DATE: 2001-10-29
; PRIOR APPLICATION NUMBER: US 09/902,941
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 09/849,626
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 09/736,457
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: US 09/702,705
; PRIOR FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: US 09/677,419
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: US 09/671,325
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/658,824
; PRIOR FILING DATE: 2000-09-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2157
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2108
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-301-554-2108

Query Match      26.0%; Score 25; DB 7; Length 14;
Best Local Similarity 45.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy      1 IDGQVDEQFP 11
      | : | : |
Db      2 IERRKIMEQSP 12

RESULT 7
US-10-522-356-9
; Sequence 9, Application US/10522356
; Publication No. US20060105323A1
; GENERAL INFORMATION:
; APPLICANT: WHITELEW, CHRISTOPHER BRUCE ALEXANDER
; APPLICANT: CLARK, ANTHONY JOHN
; APPLICANT: WOLF, CHARLES ROLAND
; TITLE OF INVENTION: MULTI-REPORTER GENE MODEL FOR TOXICOLOGICAL SCREENING
; FILE REFERENCE: 102286.155 US1
; CURRENT APPLICATION NUMBER: US/10/522,356
; PRIOR FILING DATE: 2005-01-26
; PRIOR APPLICATION NUMBER: PCT/GB03/003192
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; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: GB 0217402.7
; PRIOR FILING DATE: 2002-07-26
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 9
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of unknown Sequence: ARF
; OTHER INFORMATION: epitope from unknown organism
US-10-522-356-9

Query Match      26.0%; Score 25; DB 6; Length 16;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      8 EQFPQH 13
      | : | |
Db      8 ERFPQH 13

RESULT 8
US-11-244-348A-7
; Sequence 7, Application US/11244348A
; Publication No. US2006010493A1
; GENERAL INFORMATION:
; APPLICANT: Mreny, Randall J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IMMUNIZING
; TITLE OF INVENTION: AGAINST PSEUDOMONAS INFECTION
; FILE REFERENCE: 10901-015-999
; CURRENT APPLICATION NUMBER: US/11/244,348A
; CURRENT FILING DATE: 2005-10-04
; PRIOR APPLICATION NUMBER: 60/616,125
; PRIOR FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Pseudomonas sp.
US-11-244-348A-7

Query Match      26.0%; Score 25; DB 7; Length 17;
Best Local Similarity 54.5%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy      7 DEQFPQHGVK 17
      | : | | |
Db      7 DEQFIPKQSK 17

RESULT 9
US-11-332-378-216
; Sequence 216, Application US/11332378
; Publication No. US20060106196A1
; GENERAL INFORMATION:
; APPLICANT: Gaudernack, Gustav
; APPLICANT: Eriksen, Jon Amund
; APPLICANT: Moller, Mona
; APPLICANT: Gjertsen, Marianne Klemp
; APPLICANT: Saeterdal, Ingvil
; APPLICANT: Saebøe-Larsen, Stein
; TITLE OF INVENTION: Antigenic Peptides Derived from Telomerase
; FILE REFERENCE: 01702.401800
; CURRENT APPLICATION NUMBER: US/11/332,378
; CURRENT FILING DATE: 2006-01-17
; PRIOR APPLICATION NUMBER: US/09/743,281
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: PCT/NO99/00220
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 231
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SOFTWARE: PatentIn version 3.0
; SEQ ID NO 216
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens, other or unknown
US-11-332-378-216

Query Match 25.0%; Score 24; DB 7; Length 9;
Best Local Similarity 80.0%; Pred. No. 5.2e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 EQFPOHGL 15
Db 2 EQFKQKAL 6

RESULT 10
US-11-140-487A-794

; Sequence 794, Application US/11140487A
; Publication No. US20060093617A1
; GENERAL INFORMATION:

; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C vi

; FILE REFERENCE: 166
; CURRENT APPLICATION NUMBER: US/11/140,487A

; PRIOR FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: EP 04012951.2

; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: EP 04447239.7

; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: EP 05102441.2

; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/576,310

; PRIOR FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: US 60/622,782

; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US 60/665,395

; PRIOR FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2278

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 794

; LENGTH: 9
; TYPE: PRT

; ORGANISM: hepatitis C virus
US-11-140-487A-794

Query Match 24.0%; Score 23; DB 7; Length 9;
Best Local Similarity 62.5%; Pred. No. 5.2e+04;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 EQFPOHGL 15
Db 2 EQFKQKAL 9

RESULT 11
US-11-140-487A-795

; Sequence 795, Application US/11140487A
; Publication No. US20060093617A1
; GENERAL INFORMATION:

; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C vi

; FILE REFERENCE: 166
; CURRENT APPLICATION NUMBER: US/11/140,487A

; PRIOR FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: EP 04012951.2

; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: EP 04447239.7

; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: EP 05102441.2

; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/576,310

; PRIOR FILING DATE: 2004-06-03

; PRIOR APPLICATION NUMBER: US 60/622,782
; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US 60/665,395
; PRIOR FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2278
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 795

QY 10 EQFPOHGL 15
Db 2 EQFKQKAL 9

Query Match 24.0%; Score 23; DB 7; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 EQFPOHGL 15
Db 2 EQFKQKAL 9

RESULT 12
US-11-140-487A-1029

; Sequence 1029, Application US/11140487A
; Publication No. US20060093617A1
; GENERAL INFORMATION:

; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C vi

; FILE REFERENCE: 166
; CURRENT APPLICATION NUMBER: US/11/140,487A

; PRIOR FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: EP 04012951.2

; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: EP 04447239.7

; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: EP 05102441.2

; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/576,310

; PRIOR FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: US 60/622,782

; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US 60/665,395

; PRIOR FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2278

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1029

; LENGTH: 10
; TYPE: PRT

; ORGANISM: hepatitis C virus
US-11-140-487A-1029

Query Match 24.0%; Score 23; DB 7; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 EQFPOHGL 15
Db 1 EQFKQKAL 8

RESULT 13
US-11-122-986-542

; Sequence 542, Application US/11122986
; Publication No. US20060104989A1
; GENERAL INFORMATION:

; APPLICANT: EDWARDS, ALED
; APPLICANT: DHARAMSI, AKIL

; APPLICANT: VEDADI, MASOUD
; TITLE OF INVENTION: ESSENTIAL NOVEL BACTERIAL POLYPEPTIDES
; FILE REFERENCE: IPT-330.01

; CURRENT APPLICATION NUMBER: US/11/122,986
; PRIOR FILING DATE: 2005-05-05

; PRIOR APPLICATION NUMBER: 60/423,875

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; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,832
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,915
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,757
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,758
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/424,367
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,376
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,370
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,362
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,373
; PRIOR FILING DATE: 2002-11-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 844
; SOFTWARE: Patentln Ver. 3.3
; SEQ ID NO 542
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-11-122-986-542
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```

Query March 24.0%; Score 23; DB 7; Length 14;
Best Local Similarity 30.0%; Pred. No. 2.6e+02;
Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
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QY 4 QKVDQEPFH 13
Db 1 EELDDAFDYH 10
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```

RESULT 14
US-11-122-986-789
; Sequence 789, Application US/11122986
; Publication No. US20060104989A1
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, ALED
; APPLICANT: DHARMSI, AKIL
; APPLICANT: VEDADI, MASOUD
; TITLE OF INVENTION: ESSENTIAL NOVEL BACTERIAL POLYPEPTIDES
; FILE REFERENCE: IPT-330.01
; CURRENT APPLICATION NUMBER: US/11/122,986
; PRIOR FILING DATE: 2005-05-05
; PRIOR APPLICATION NUMBER: 60/423,875
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,832
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,915
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,757
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,758
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/424,367
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,376
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,370
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,362
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,373
; PRIOR FILING DATE: 2002-11-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 844
; SOFTWARE: Patentln Ver. 3.3
; SEQ ID NO 789
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```

; LENGTH: 9
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-11-122-986-789
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Query March 22.9%; Score 22; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.2e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```
QY 10 FPOHGL 15
Db 3 FPEVGL 8
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```

RESULT 15
US-11-122-986-673
; Sequence 673, Application US/11122986
; Publication No. US20060104989A1
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, ALED
; APPLICANT: DHARMSI, AKIL
; APPLICANT: VEDADI, MASOUD
; TITLE OF INVENTION: ESSENTIAL NOVEL BACTERIAL POLYPEPTIDES
; FILE REFERENCE: IPT-330.01
; CURRENT APPLICATION NUMBER: US/11/122,986
; PRIOR FILING DATE: 2005-05-05
; PRIOR APPLICATION NUMBER: 60/423,875
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,832
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,915
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,757
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,758
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/424,367
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,376
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,370
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,362
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,373
; PRIOR FILING DATE: 2002-11-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 844
; SOFTWARE: Patentln Ver. 3.3
; SEQ ID NO 673
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-11-122-986-673
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Query March 22.9%; Score 22; DB 7; Length 11;
Best Local Similarity 40.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
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QY 3 GOKVDEQFPQ 12
Db 2 GKLDDEDMWR 11
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Job time : 4 secs
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OM protein - protein search, using sw model

Run on: May 30, 2006, 15:08:01 ; Search time 19.3333 Seconds
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Title: US-10-758-165A-11
Sequence score: 96
Sequence: 1 IDGQKVDGEPFGHGVKQ 18

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Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 271358

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	35.4	15	2	US-08-914-479A-11 Sequence 11, Appl
2	32	33.3	10	1	US-08-151-574-3 Sequence 3, Appl
3	32	33.3	10	1	US-08-419-448-3 Sequence 3, Appl
4	32	33.3	10	2	US-09-233-510-3 Sequence 8, Appl
5	30	31.2	11	1	US-08-486-839-8 Sequence 8, Appl
6	30	31.2	11	2	US-09-151-011-8 Sequence 8, Appl
7	30	31.2	11	2	US-09-343-623-8 Sequence 8, Appl
8	30	31.2	11	2	US-09-977-827-8 Sequence 8, Appl
9	29	30.2	9	3	US-09-743-281C-136 Sequence 136, App
10	29	30.2	10	1	US-08-166-195A-23 Sequence 23, Appl
11	29	30.2	10	1	US-08-436-772-23 Sequence 23, Appl
12	29	30.2	10	1	US-08-436-883B-23 Sequence 23, Appl
13	29	30.2	11	1	US-08-486-839-12 Sequence 12, Appl
14	29	30.2	11	2	US-09-151-011-12 Sequence 12, Appl
15	29	30.2	11	2	US-09-343-623-12 Sequence 12, Appl
16	29	30.2	11	2	US-09-977-827-13 Sequence 13, Appl
17	29	30.2	11	2	US-09-977-827-13 Sequence 13, Appl
18	29	30.2	15	1	US-08-006-341-2 Sequence 2, Appl
19	28	29.2	16	2	US-09-511-625B-64 Sequence 64, Appl
20	28	29.2	15	1	US-07-995-503A-10 Sequence 10, Appl
21	28	29.2	15	1	US-08-390-510-10 Sequence 10, Appl
22	28	29.2	15	1	US-08-390-790-10 Sequence 10, Appl
23	28	29.2	15	1	US-08-390-509-10 Sequence 10, Appl
24	28	29.2	15	2	US-09-149-860A-10 Sequence 10, Appl
25	28	29.2	17	2	US-08-836-561-41 Sequence 41, Appl
26	27	28.1	10	2	US-09-434-122-41 Sequence 41, Appl
27	27	28.1	10	2	US-08-371-660-10 Sequence 10, Appl

27	27	28.1	11	1	US-08-486-839-14	Sequence 14, Appl
28	27	28.1	11	2	US-09-151-011-14	Sequence 14, Appl
29	27	28.1	11	2	US-09-343-623-14	Sequence 14, Appl
30	27	28.1	11	2	US-09-977-827-15	Sequence 15, Appl
31	27	28.1	15	2	US-08-475-955-75	Sequence 75, Appl
32	27	28.1	15	2	US-07-867-819D-75	Sequence 75, Appl
33	27	28.1	16	2	US-07-701-588C-107	Sequence 107, App
34	27	28.1	11	1	US-08-486-839-13	Sequence 13, Appl
35	26	27.1	11	2	US-08-151-011-13	Sequence 13, Appl
36	26	27.1	11	2	US-09-343-623-13	Sequence 13, Appl
37	26	27.1	11	2	US-09-685-010-49	Sequence 13, Appl
38	26	27.1	11	2	US-09-977-827-14	Sequence 14, Appl
39	26	27.1	11	2	US-09-978-309A-49	Sequence 49, Appl
40	26	27.1	11	2	US-09-978-309A-84	Sequence 84, Appl
41	26	27.1	12	1	US-08-151-574-9	Sequence 9, Appl
42	26	27.1	12	1	US-08-196-940-3	Sequence 9, Appl
43	26	27.1	12	1	US-08-419-448-9	Sequence 9, Appl
44	26	27.1	12	2	US-09-233-510-9	Sequence 9, Appl
45	26	27.1	12	2	US-09-685-010-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-08-914-479A-11
Sequence 11, Application US/08914479A
Patent No. 6419932
GENERAL INFORMATION:
APPLICANT: Dale, James B.
TITLE OF INVENTION: ANTIGEN OF HYBRID M PROTEIN AND CARRIER
FILE REFERENCE: 481112.404C2
CURRENT FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 08/409,270
PRIOR FILING DATE: 1995-03-23
PRIOR APPLICATION NUMBER: 07/945,860
PRIOR FILING DATE: 1992-09-16
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: NH2-terminal fragment of M protein for
OTHER INFORMATION: constructing antigen, which elicit opsonic
OTHER INFORMATION: antibodies in an immunized animal
US-08-914-479A-11
Query Match 35.4%; Score 34; DB 2; Length 15;
Best Local Similarity 41.7%; Pred. No. 27;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 2 DGQKVDGEPFGH 13
Db 1 DARSNGEPPRH 12
US-08-151-574-3
Sequence 3, Application US/08151574
Patent No. 5436156
GENERAL INFORMATION:
APPLICANT: Robert F.M. Van Gorcom
APPLICANT: Willem Van Hartingsveldt
APPLICANT: Petrus A. Van Paridon
APPLICANT: Annemarie E. Veestra
APPLICANT: Rudolf G.M. Luttin
APPLICANT: Gerardus Seltien
TITLE OF INVENTION: Cloning and Expression of Microbial
TITLE OF INVENTION: Phytase

```

;
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/151,574
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/688,578
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20026.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; FRAGMENT TYPE: N-terminal
;
; US-08-151-574-3
;
Query Match 33.3%; Score 32; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 VDEQFPQHG 14
   |||:| |
Db 2 VDERFPYTG 10

RESULT 3
; US-08-419-448-3
; Sequence 3, Application US/08419448
; Patent No. 5863533
;
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Sellen
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 2000 Pennsylvania Ave. N.W., Suite 5500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006-1888
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,448
; FILING DATE: 10-APR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20026.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-887-1500
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; FRAGMENT TYPE: N-terminal
;
; US-08-419-448-3
;
Query Match 33.3%; Score 32; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 VDEQFPQHG 14
   |||:| |
Db 2 VDERFPYTG 10

RESULT 4
; US-09-233-510-3
; Sequence 3, Application US/09233510
; Patent No. 6350602
;
; GENERAL INFORMATION:
; APPLICANT: Robert F.M. Van Gorcom
; APPLICANT: Willem Van Hartingsveldt
; APPLICANT: Petrus A. Van Paridon
; APPLICANT: Annemarie E. Veenstra
; APPLICANT: Rudolf G.M. Luttin
; APPLICANT: Gerardus Sellen
; TITLE OF INVENTION: Cloning and Expression of Microbial
; TITLE OF INVENTION: Phytase
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 545 Middlefield Road, Suite 200
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-3471
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/233,510
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/688,578
; FILING DATE: 24-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Murashige, Kate H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20026.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-327-7250
; TELEFAX: 415-327-2951
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
;
;

```

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
FRAGMENT TYPE: N-terminal
US-09-233-510-3

Query Match 33.3%; Score 32; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 VDEQFQHG 14
Db 2 VDERFPYTG 10

RESULT 5
US-08-486-839-8
Sequence 8, Application US/08486839
Patent No. 5928928
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: A human chitinase, its recombinant
TITLE OF INVENTION: production, its use for decomposing chitin, its use
NUMBER OF INVENTION: in therapy or prophylaxis against infection diseases.
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann & Baron
STREET: 350 Jericho Turnpike
CITY: Jericho
STATE: New York
COUNTRY: United States of America
ZIP: 11758
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,839
FILING DATE: 07 - June - 1995
ATTORNEY/AGENT INFORMATION:
NAME: Baron, Ronald J.
REGISTRATION NUMBER: 29,281
REFERENCE/DOCKET NUMBER: 294-26
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 822-3550
TELEFAX: (516) 822-3582
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHEICAL: NO
US-08-486-839-8

Query Match 31.2%; Score 30; DB 1; Length 11;
Best Local Similarity 50.0%; Pred. No. 93;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DGQKVDEQFP 11
Db 2 DGVIDWEFP 11

RESULT 6
US-09-151-011-8
Sequence 8, Application US/09151011
Patent No. 6057142
GENERAL INFORMATION:

APPLICANT:
TITLE OF INVENTION: A Human Chitinase, Its Recombinant
TITLE OF INVENTION: Production, its use for decomposing chitin, its use in
TITLE OF INVENTION: Therapy or Prophylaxis Against Infection Diseases.
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann & Baron, LLP
STREET: 6900 Jericho Turnpike
CITY: Syosset
STATE: New York
COUNTRY: United States of America
ZIP: 11791
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/151,011
FILING DATE: 10 - September - 1998
ATTORNEY/AGENT INFORMATION:
NAME: Morris, Robert C.
REGISTRATION NUMBER: 42,910
REFERENCE/DOCKET NUMBER: 294-32 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 822-3550
TELEFAX: (516) 822-3582
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHEICAL: NO
US-09-151-011-8

Query Match 31.2%; Score 30; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 93;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DGQKVDEQFP 11
Db 2 DGVIDWEFP 11

RESULT 7
US-09-343-623-8
Sequence 8, Application US/09343623
Patent No. 6303118
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: A human chitinase, its recombinant
TITLE OF INVENTION: production, its use for decomposing chitin, its use
NUMBER OF INVENTION: in therapy or prophylaxis against infection diseases.
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann & Baron
STREET: 350 Jericho Turnpike
CITY: Jericho
STATE: New York
COUNTRY: United States of America
ZIP: 11758
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/343,623
FILING DATE:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/486,839
FILING DATE: 07-June-1995
ATTORNEY/AGENT INFORMATION:
NAME: Barton, Ronald J.
REGISTRATION NUMBER: 29,281
REFERENCE/DOCKET NUMBER: 294-26
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 822-3550
TELEFAX: (516) 822-3582
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-09-343-623-8

Query Match 31.2%; Score 30; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 93;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DGQKVDQFP 11
|||:|
Db 2 DGVDIDWEP 11

RESULT 8
US-09-977-827-8
Sequence 8, Application US/09977827
Patent No. 6896884
GENERAL INFORMATION:
APPLICANT: Aerts, Johannes Maria F.G.
TITLE OF INVENTION: A human chitinase, its recombinant production, its use for decomp
FILE REFERENCE: Docket 294-32 DIVII/CON
CURRENT APPLICATION NUMBER: US/09/977,827
CURRENT FILING DATE: 2001-10-15
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.1
SEQ ID NO 8
LENGTH: 11
TYPE: PRT
ORGANISM: Autographa californica
US-09-977-827-8

Query Match 31.2%; Score 30; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 93;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DGQKVDQFP 11
|||:|
Db 2 DGVDIDWEP 11

RESULT 9
US-09-743-281C-136
Sequence 136, Application US/09743281C
Patent No. 7030211
GENERAL INFORMATION:
APPLICANT: Gaudernack, Gustav
APPLICANT: Eriksen, Jon Amund
APPLICANT: Moller, Mona
APPLICANT: Gjertsen, Marianne Klomp
APPLICANT: Saeterdal, Ingvil
APPLICANT: Saebøe-Larsen, Stein
TITLE OF INVENTION: Antigenic Peptides Derived from Telomerase
FILE REFERENCE: 01702,401800
CURRENT APPLICATION NUMBER: US/09/743,281C
CURRENT FILING DATE: 2001-07-05
PRIOR APPLICATION NUMBER: PCT/NO99/00220

PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 231
SOFTWARE: PatentIn version 3.0
SEQ ID NO 136
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens, other or unknown
US-09-743-281C-136

Query Match 30.2%; Score 29; DB 3; Length 9;
Best Local Similarity 71.4%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 QPQHGL 15
|||:|
Db 3 QMPAHGL 9

RESULT 10
US-08-166-195A-23
Sequence 23, Application US/08166195A
Patent No. 5480799
GENERAL INFORMATION:
APPLICANT: O'Rand, Michael G.
APPLICANT: Widsren, Esther E.
APPLICANT: Richardson, Richard T.
APPLICANT: Lea, Isabel
TITLE OF INVENTION: Sperm Antigen Corresponding to a
TITLE OF INVENTION: Sperm Zona Binding Protein Autoantigenic Epitope
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenneth D. Sibley
STREET: P.O. Box 34009
CITY: Charlotte
STATE: No. 5480799th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/166,195A
FILING DATE: 10 DEC 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470/73
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-166-195A-23

Query Match 30.2%; Score 29; DB 1; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 GQKVDQFP 10
|||:|
Db 1 GAKVDQFP 8

RESULT 11
US-08-436-772-23

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; Sequence 23, Application US/08436772
; Patent No. 5814456
; GENERAL INFORMATION:
; APPLICANT: O'Rand, Michael G.
; APPLICANT: Widdgren, Esther E.
; APPLICANT: Richardson, Richard T.
; APPLICANT: Lea, Isabel
; TITLE OF INVENTION: Sperm Antigen Corresponding to a Sperm
; TITLE OF INVENTION: Zona Binding Protein Autoantigenic Epitope
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: P.O. Box 34009
; CITY: Charlotte
; STATE: No. 5814456th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,772
; FILING DATE: 08-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-73B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-881-3140
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-436-772-23

Query Match 30.2%; Score 29; DB 1; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GAKYDEQF 10
Db 1 GAKYDDRF 8

RESULT 12
US-08-436-883B-23
; Sequence 23, Application US/0843683B
; Patent No. 5820861
; GENERAL INFORMATION:
; APPLICANT: O'Rand, Michael G.
; APPLICANT: Widdgren, Esther E.
; APPLICANT: Richardson, Richard T.
; APPLICANT: Lea, Isabel
; TITLE OF INVENTION: Sperm Antigen Corresponding to a Sperm
; TITLE OF INVENTION: Zona Binding Protein Autoantigenic Epitope
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: P.O. Box 34009
; CITY: Charlotte
; STATE: No. 5820861th Carolina
; COUNTRY: USA
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,883B
; FILING DATE: 08-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5470-73C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-420-2200
; TELEFAX: 919-881-3175
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-436-883B-23

Query Match 30.2%; Score 29; DB 1; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GAKYDEQF 10
Db 1 GAKYDDRF 8

RESULT 13
US-08-486-839-12
; Sequence 12, Application US/08486839
; Patent No. 5928928
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: A human chitinase, its recombinant
; TITLE OF INVENTION: production, its use for decomposing chitin, its use
; TITLE OF INVENTION: in therapy or prophylaxis against infection diseases.
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann & Baron
; STREET: 350 Jericho Turnpike
; CITY: Jericho
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11758
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,839
; FILING DATE: 07 - June - 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Baron, Ronald J.
; REGISTRATION NUMBER: 29,281
; REFERENCE/DOCKET NUMBER: 294-26
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 822-3550
; TELEFAX: (516) 822-3582
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; US-08-486-839-12
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Query Match	30.2%	Score 29	DB 1	Length 11
Best Local Similarity	50.0%	Pred. No. 1.4e+02		
Matches	5	Conservative	2	Mismatches 3
				Indels 0
				Gaps 0
QY	2	DGQKVDDEQF	11	
		: : :		
Db	2	DGLNLDWQYP	11	

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RESULT 14
US-09-151-011-12
; Sequence 12, Application US/09151011
; Patent No. 6057142
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: A Human Chitinase, Its Recombinant
; TITLE OF INVENTION: Production, Its Use For Decomposing Chitin, Its Use in
; TITLE OF INVENTION: Therapy or Prophylaxis Against Infection Diseases.
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann & Baron, LLP
; STREET: 6900 Jericho Turnpike
; CITY: Syosset
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11791
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; SOFTWARE:
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/151,011
; FILING DATE: 10 - September - 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Morris, Robert C.
; REGISTRATION NUMBER: 42,910
; REFERENCE/DOCKET NUMBER: 294-32 DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 822-3550
; TELEFAX: (516) 822-3582
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; / HYPOTHETICAL: NO
US-09-151-011-12

Query Match 30.2%; Score 29; DB 2; length 11;
Best Local Similarity 50.0%; Pred.No. 14+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DQGVDEQFP 11
|| : || : ||
Db 2 DGLNLDWQYP 11

RESULT 15
US-09-343-623-12
; Sequence 12, Application US/09343623
; Patent No. 6303118
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: A human chitinase, its recombinant
; TITLE OF INVENTION: production, its use for decomposing chitin, its use
; TITLE OF INVENTION: in therapy or prophylaxis against infection diseases.
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:

```

```

? ADDRESS: Hoffmann & Baron
? STREET: 350 Jericho Turnpike
? CITY: Jericho
? STATE: New York
? COUNTRY: United States of America
? ZIP: 11758
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent'n Release #1.0, Version #1.30
? SOFTWARE:
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/343,623
? FILING DATE:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US/08/486,839
? FILING DATE: 07-June-1995
? ATTORNEY/AGENT INFORMATION:
? NAME: Baron, Ronald J.
? REGISTRATION NUMBER: 29,281
? REFERENCE/DOCKET NUMBER: 294-26
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (516) 822-3550
? TELEFAX: (516) 822-3582
? INFORMATION FOR SEQ ID NO: 12:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 11 amino acids
? TYPE: amino acid
? STRANDEDNESS: unknown
? TOPOLOGY: unknown
? MOLECULE TYPE: Protein
? HYPOTHEICAL: NO
? US-09-343-12

Query Match 30.2%; Score 29; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DGQKVDKDFP 11
DB 2 DGLNDWDQYF 11

```

Search completed: May 30, 2006, 15:09:24
Job time : 19.3333 secs

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Query Match      30.2%; Score 29; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches      5; Conservative      2; Mismatches      3; Indels      0;
OY      2 DGQKVD E QFP 11
      ||| : |||
Db      2 DGLNLDMQYP 11

```

Search completed: May 30, 2006, 15:09:24
Job time : 19.3333 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 30, 2006, 15:04:28 ; Search time 12 Seconds
(without alignments)
144.325 Million cell updates/sec

Title: US-10-758-165A-10

Perfect score: 97

Sequence: 1 VDCGKATNIPFYTPAGKQ 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3215

Minimum DB seq length: 0

Maximum DB seq length: 18

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.80:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27.8	17	2	H49048	T-cell receptor be
2	27.8	18	2	A59137	protein p11 - gold
3	26.8	18	2	A61577	24k serine protein
4	24.7	14	2	B58502	36k kidney strom p
5	24.7	17	2	S18534	hypothetical prote
6	23.7	12	2	P00786	NADH2 dehydrogenas
7	23.7	15	2	B45115	peptidylprolyl iso
8	23.7	18	2	S20322	gluten - wheat
9	22.7	12	2	P01700	alcohol dehydrogen
10	22.7	13	2	S01904	H+-transporting tw
11	22.7	15	2	PA0056	protein QP200002 -
12	22.7	15	2	PA0087	cytochrome c2 - fu
13	22.7	15	2	PA0099	phenocytic variati
14	22.7	16	2	A28144	ribosomal protein
15	22.7	17	2	C84063	hypothetical prote
16	22.7	18	2	C56046	urinary tract ston
17	22.7	10	2	S71948	matrix metalloprot
18	21.6	10	2	A19745	endo-glucosylceram
19	21.6	11	2	A34135	DNA-binding protei
20	21.6	12	2	A53524	ubiquitinol-cytochr
21	21.6	14	2	PL0142	carbon-monoxide de
22	21.6	14	2	S59495	formate dehydrogen
23	21.6	15	2	B61457	alpha-glucosidase
24	21.6	16	2	B53284	T-cell receptor be
25	21.6	16	2	S38292	30k allergen - rye
26	21.6	17	2	S50901	chlorophyll a/b-bi
27	21.6	18	2	S57518	T cell receptor be
28	21.6	18	2	S70612	alpha-macroglobuli
29	20.5	18	2	A28027	protein p2 - curle

30	20	20.6	9	2	S59902	glutathione transf
31	20	20.6	9	2	D48186	ATPase R1 subunit
32	20	20.6	9	2	S10784	enamelin 1 - bovin
33	20	20.6	13	2	B58533	CD61 homolog - cha
34	20	20.6	14	2	S22236	lipoxigenase (EC 1
35	20	20.6	14	2	S19803	ubiquitin - potato
36	20	20.6	14	2	PA0109	porin por 1B - Ara
37	20	20.6	14	2	G44957	photosystem II oxy
38	20	20.6	14	2	PH1306	lg heavy chain DQ
39	20	20.6	14	2	PA0045	porin por1 - Arabi
40	20	20.6	14	2	S12904	protein kinase (EC
41	20	20.6	15	2	PA0097	starch phosphoryla
42	20	20.6	15	2	S71300	ICU3 protein - Par
43	20	20.6	15	2	PS0455	superoxide dismuta
44	20	20.6	15	2	PA0063	ubiquitin - fungus
45	20	20.6	15	2	A49177	22k protein p1, mi

ALIGNMENTS

RESULT 1
H49048
T-cell receptor beta chain V region (CDR3 junction, clone Vbeta20.1) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 21-Jan-1994 #sequence #revision 18-Nov-1994 #text_change 30-May-1997
C:Accession: H49048
R:Stoud, M.; Kjeldsen-Kragh, J.; Suleyman, S.; Vinje, O.; Natvig, J.B.; Forre, O.
Eur. J. Immunol. 22, 2413-2418, 1992
A:Title: Limited heterogeneity of T cell receptor variable region gene usage in juvenile
A:Reference number: H49048; MUID:92387250; PMID:1387614
A:Accession: H49048
A:Status: Preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-17 <SIO>
A:Cross-references: UNIPARC:UPI0000176DFO
A:Experimental source: patient SS, IL-2R+ syrovial T-cells
A>Note: sequence extracted from NCBI backbone (NCBI:113270)
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: T-cell receptor

Query Match 27.8% Score 27; DB 2; Length 17;
Best Local Similarity 62.5%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 ATNIFPYT 13
DB 8 AWTFFPYT 15

RESULT 2
A59137
protein p11 - golden needle mushroom (fragment)
C:Species: Flammulina velutipes (golden needle mushroom)
C:Date: 12-Nov-1999 #sequence #revision 12-Nov-1999 #text_change 09-Jul-2004
C:Accession: A59137
R:Sakamoto, Y.; Ando, A.; Tamai, Y.; Miura, K.
submitted to the Protein Sequence Database, November 1999
A:Description: Differences of proteins expressed in the fruiting dikaryon and the non-fr
A:Reference number: A59137
A:Accession: A59137
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-18 <SAK>
A:Cross-references: UNIPROT:Q7M4W6; UNIPARC:UPI000017CB27

Query Match 27.8% Score 27; DB 2; Length 18;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 PYTAP 15
DB 2 PYTSP 6

RESULT 3

A61577
24k serine proteinase (EC 3.4.21.-) - Streptomyces fradiae (fragment)
C:Species: Streptomyces fradiae
C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C:Accession: A61577
R:Sinha, U.; Molz, S.A.; Lad, P.J.
Int. J. Biochem. 23, 979-984, 1991
A:Title: Two new extracellular serine proteases from Streptomyces fradiae.
A:Reference number: A61577; MUID:92155439; PMID:1786859
A:Accession: A61577
A:Molecule type: protein
A:Residues: 1-18 <SIN>
A:Cross-references: UNIPROT:Q7M198; UNIPARC:UPI000017AB13
C:Keywords: extracellular protein; hydrolase; serine proteinase

Query Match 26.8%; Score 26; DB 2; Length 18;
Best Local Similarity 41.7%; Pred. No. 5.6e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Oy 1 VDQKATNIPY 12
|||
Db 2 VGTTRAAQEPWP 13

RESULT 4

B58502
36k kidney stone protein - unidentified bacterium (fragment)
C:Species: unidentified bacterium
C:Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 10-Jul-1998
C:Accession: B58502
R:Binette, J.P.; Binette, M.B.
submitted to the Protein Sequence Database, October 1996
A:Description: The proteins of kidney and gallbladder stones.
A:Reference number: A58501
A:Accession: B58502
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <BIN>
A:Cross-references: UNIPARC:UPI000017ABD0
A:Experimental source: human kidney stone containing Ca ox.monoh dihyd, 1% struvite, CaH
A:Note: tentative identification of 8-Tyr and 9-Thr

Query Match 24.7%; Score 24; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 9.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 8 NIPPYT 13
|||
Db 4 NLPFYT 9

RESULT 5

S18534
hypothetical protein 7 (eryG 3' region) - Saccharopolyspora erythraea (fragment)
C:Species: Saccharopolyspora erythraea
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 07-Apr-1994
C:Accession: S18534
R:Haydock, S.F.; Dowson, J.A.; Dhillon, N.; Roberts, G.A.; Cortes, J.; Leadlay, P.F.
Mol. Gen. Genet. 230, 120-128, 1991
A:Title: Cloning and sequence analysis of genes involved in erythromycin biosynthesis in
methyltransferases.
A:Reference number: S18530; MUID:92079886; PMID:1840640
A:Accession: S18534
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-17 <HAY>
A:Cross-references: UNIPARC:UPI000017ADB1; EMBL:X60379
A:Note: the authors translated the codon CTG for residue 12 as Gly

Query Match 24.7%; Score 24; DB 2; Length 17;

Best Local Similarity 62.5%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 9 IFPYTAPG 16
|||
Db 1 IFPAVAGS 8

RESULT 6

P00786
NADH2 dehydrogenase (EC 1.6.99.3) 26k chain - fava bean mitochondrion (fragment)
N:Alternate names: complex I 26k chain; NADH-ubiquinone reductase 26k chain
C:Species: mitochondrion Vicia faba (fava bean)
C:Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C:Accession: P00786
R:Jeterme, S.; Boulter, M.
Plant Physiol. 102, 435-443, 1993
A:Title: Purification and preliminary characterization of mitochondrial complex I (NADH:
A:Reference number: P00775; MUID:94151437; PMID:8108509
A:Accession: P00786
A:Molecule type: protein
A:Residues: 1-12 <LET>
A:Cross-references: UNIPROT:Q7M2G3; UNIPARC:UPI000017CPA8
C:Comment: Complex I, mitochondrial NADH-ubiquinone reductase, is the first of the ch
ranging from 5K to 75K.
C:Comment: This enzyme catalyzes electron transfer from endogenous NADH to ubiquinone by

A:Genome: mitochondrion
C:Keywords: electron transfer; mitochondrion; oxidoreductase

Query Match 23.7%; Score 23; DB 2; Length 12;
Best Local Similarity 53.8%; Pred. No. 1.2e+03;
Matches 7; Conservative 2; Mismatches 2; Indels 2; Gaps 2;

Oy 6 ATNI-FPYTAPGK 17
|||
Db 1 ATGVPIPY-APGE 12

RESULT 7

B45115
peptidylprolyl isomerase (EC 5.2.1.8) FKBP51 - human (fragment)
N:Alternate names: FK506-binding protein FKBP51; peptidylprolyl cis-trans isomerase FKBP
C:Species: Homo sapiens (man)
C:Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: B45115
R:Wiederecht, G.; Hung, S.; Chan, H.K.; Marcy, A.; Martin, M.; Calaycay, J.; Boulton, D
J. Biol. Chem. 267, 21753-21760, 1992
A:Title: Characterization of high molecular weight FK-506 binding activities reveals a n
A:Reference number: A45115; MUID:93016131; PMID:1363226
A:Accession: B45115
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <WIE>
A:Cross-references: UNIPROT:Q9UDK1; UNIPARC:UPI0000035473
A:Experimental source: JURKAT cells
A:Note: sequence extracted from NCBI backbone (NCBIP:116748)
C:Keywords: cis-trans-isomerase; cyclosporin A binding

Query Match 23.7%; Score 23; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 6 ATNIPFYTAP 15
|||
Db 1 ATESIAVYLP 10

RESULT 8

S20322
gluten - wheat
C:Species: Triticum aestivum (common wheat)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C;Accession: S20322
 R;Fukudome, S.; Yoshikawa, M.
 FEBS Lett. 296, 107-111, 1992
 A;Title: Opioid peptides derived from wheat gluten: their isolation and characterization
 A;Reference number: S20322; MUID:92111773; PMID:1309704
 A;Accession: S20322
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-18 <FUK>
 A;Cross-references: UNIPROT:Q7MIG0; UNIPARC:UPI000017B139

Query Match 23.7%; Score 23; DB 2; Length 18;
 Best Local Similarity 40.0%; Pred. No. 1.8e+03;
 Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 GQKATNIPY 12
 |||:
 1 GYPTGYVY 10

Db

RESULT 9
 PN0170
 alcohol dehydrogenase (EC 1.1.1.1) - fungus (Fusarium sporotrichioides) (fragment)
 C;Species: Fusarium sporotrichioides
 C;Date: 05-Aug-1994 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
 C;Accession: PN0170
 R;Fukaya, N.; Chow, L.P.; Sugiyura, Y.; Tsugita, A.; Ueno, Y.; Tabuchi, K.
 submitted to JIPID, May 1994
 A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich
 A;Reference number: PN0160
 A;Accession: PN0170
 A;Molecule type: protein
 A;Residues: 1-12 <FUK>
 A;Cross-references: UNIPROT:Q7M4Z9; UNIPARC:UPI000017B3F6
 A;Experimental source: strain M-1-1
 C;Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match 22.7%; Score 22; DB 2; Length 12;
 Best Local Similarity 66.7%; Pred. No. 1.7e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 YTAGK 17
 |||:
 6 YVDGK 11

Db

RESULT 10
 S01904
 H+-transporting two-sector ATPase (EC 3.6.3.14) beta chain - Arabidopsis thaliana chloro
 C;Species: chloroplast Arabidopsis thaliana (mouse-ear cress)
 C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
 C;Accession: S01904
 R;Chen, H.C.; Wintz, H.; Well, J.H.; Pillay, D.T.N.
 Nucleic Acids Res. 16, 10372, 1988
 A;Title: Nucleotide sequence of chloroplast CFI-ATPase epsilon-subunit and elongator tRN
 A;Reference number: S01903; MUID:89057486; PMID:2904134
 A;Accession: S01904
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-13 <CHE>
 A;Cross-references: UNIPROT:P19366; UNIPARC:UPI000016D348; EMBL:X12889; NID:g11332; PDK
 C;Genetics:
 A;Gene: atpB
 A;Genome: chloroplast
 C;Keywords: ATP biosynthesis; chloroplast; hydrolase; thylakoid

Query Match 22.7%; Score 22; DB 2; Length 13;
 Best Local Similarity 80.0%; Pred. No. 1.9e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 KATNI 9
 |||:
 1 KATNL 5

Db

RESULT 11
 PA0056
 protein QP200002 - fungus (Fusarium sporotrichioides) (fragment)
 C;Species: Fusarium sporotrichioides
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
 C;Accession: PA0056
 R;Chow, L.P.; Fukaya, N.; Sugiyura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
 submitted to JIPID, October 1994
 A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich
 A;Reference number: PA0051
 A;Accession: PA0056
 A;Molecule type: protein
 A;Residues: 1-15 <CHO>
 A;Cross-references: UNIPARC:UPI000017B408

Query Match 22.7%; Score 22; DB 2; Length 15;
 Best Local Similarity 80.0%; Pred. No. 2.2e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 ATNIF 10
 |||:
 11 ATNIF 15

Db

RESULT 12
 PA0087
 cytochrome c2 - fungus (Fusarium sporotrichioides) (fragment)
 C;Species: Fusarium sporotrichioides
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
 C;Accession: PA0087
 R;Chow, L.P.; Fukaya, N.; Sugiyura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
 submitted to JIPID, October 1994
 A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich
 A;Reference number: PA0051
 A;Accession: PA0087
 A;Molecule type: protein
 A;Residues: 1-15 <CHO>
 A;Cross-references: UNIPROT:Q7M4Z7; UNIPARC:UPI000017B3F8
 C;Keywords: electron transfer; heme; photosynthesis

Query Match 22.7%; Score 22; DB 2; Length 15;
 Best Local Similarity 44.4%; Pred. No. 2.2e+03;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DGKATNIF 10
 |||:
 4 DKKGNLIF 12

Db

RESULT 13
 PA0099
 phenolic variation protein - fungus (Fusarium sporotrichioides) (fragment)
 C;Species: Fusarium sporotrichioides
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
 C;Accession: PA0099
 R;Chow, L.P.; Fukaya, N.; Sugiyura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
 submitted to JIPID, October 1994
 A;Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich
 A;Reference number: PA0051
 A;Accession: PA0099
 A;Molecule type: protein
 A;Residues: 1-15 <CHO>
 A;Cross-references: UNIPROT:Q7M4Y7; UNIPARC:UPI000017B405

Query Match 22.7%; Score 22; DB 2; Length 15;
 Best Local Similarity 57.1%; Pred. No. 2.2e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 FPYTAPG 16
 |||:
 7 FKYSASG 13

Db

RESULT 14

A28144
 ribosomal protein S27a - bovine (fragment)
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 09-Jul-2004
 C/Accession: A28144
 R/Redman, K.L.; Rechsteiner, M.
 J. Biol. Chem. 263, 4926-4931, 1988
 A/Title: Extended reading frame of a ubiquitin gene encodes a stable, conserved, basic P
 A/Reference number: A28144; MUID:88169619; PMID:2832412
 A/Accession: A28144
 A/Molecule type: protein
 A/Residues: 1-16 <RED>
 A/Cross-references: UNIPROT:O97577; UNIPARC:UPI0000177161
 C/Superfamily: ubiquitin / rat ribosomal protein S27a; ribosomal protein S27a homology;
 C/Keywords: protein biosynthesis

Query Match

Best Local Similarity 22.7%; Score 22; DB 2; Length 16;
 Pred. No. 2.4e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 YTPPK 17

Db 9 YTPPK 14

RESULT 15

C84063
 hypothetical protein BH3107 (imported) - Bacillus halodurans (strain C-125)
 C/Species: Bacillus halodurans
 C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
 C/Accession: C84063
 R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
 Nucleic Acids Res. 28, 4317-4331, 2000
 A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
 A/Reference number: A83650; MUID:20512582; PMID:11058132
 A/Accession: C84063
 A/Status: Preliminary
 A/Molecule type: DNA
 A/Residues: 1-17 <STO>
 A/Cross-references: UNIPROT:Q9K7Q4; UNIPARC:UPI00000C4168; GB:AP001518; GB:BA000004; NID
 A/Experimental source: strain C-125
 C/Genetics:
 A/Gene: BH3107

Query Match

Best Local Similarity 22.7%; Score 22; DB 2; Length 17;
 Pred. No. 2.6e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 DGKATN 8

Db 10 DNKKQTN 16

Search completed: May 30, 2006, 15:08:21
 Job time : 12 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 30, 2006, 15:01:11 ; Search time 68.6667 Seconds
(without alignments)
242.480 Million cell updates/sec

Title: US-10-758-165A-10

Perfect score: 97
Sequence: 1 VDGOKATNIPFYTAPGKQ 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 12648

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 7.2: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	35.1	17	2	046473_FELCA
2	32	33.0	8	2	Q70Y88_GLAMI
3	28.5	29.4	18	2	Q9TWL4_LUCCU
4	27.5	28.4	16	2	Q8L1Y7_PLEBO
5	27	27.8	18	2	Q7M4W6_FLEAVE
6	26	26.8	15	2	Q7S007_NEUCR
7	26	26.8	18	2	Q7M198_STRFR
8	25	25.8	15	1	CWP16_LYCES
9	25	25.8	15	2	Q9UR63_EMENT
10	25	25.8	16	2	Q3ZEV4_GCHAR
11	24	24.7	14	2	Q714T5_9CRYP
12	24	24.7	16	2	Q7TPH9_PROSU
13	24	24.7	16	2	Q3ZEY6_9CHAR
14	24	24.7	17	2	Q65Y26_HORSE
15	24	24.7	18	2	Q3TW38_MOUSE
16	23	23.7	10	2	Q9Z1B1_CLODI
17	23	23.7	12	2	Q7M2G3_VICFA
18	23	23.7	14	1	CWP27_TOBAC
19	23	23.7	14	2	P78359_HUMAN
20	23	23.7	15	2	Q5D4R7_9CYAN
21	23	23.7	16	2	Q8L1Y8_9CYAN
22	23	23.7	16	2	Q89560_HHV8
23	23	23.7	17	2	Q9TWB9_ACACA
24	23	23.7	17	2	Q9PRU8_CHICK
25	23	23.7	18	2	Q7M1G0_WHEAT
26	22	22.7	8	2	Q59AB6_HUMAN
27	22	22.7	10	2	Q71VN2_MOUSE
28	22	22.7	10	2	Q9QVE9_9MURI
29	22	22.7	11	1	PVK1_PERYR
30	22	22.7	12	2	Q7M4Z9_FUSSP
31	22	22.7	14	2	Q70Y94_GLAMI

32	22	22.7	15	2	Q7M4V7_FUSAP	Q7M4V7_fusarium sp
33	22	22.7	15	2	Q7M4Z7_FUSSP	Q7M4Z7_fusarium sp
34	22	22.7	15	2	Q9TRB5_BOVIN	Q9TRB5_bos taurus
35	22	22.7	15	2	Q9TRN8_PIG	Q9TRN8_sus scrofa
36	22	22.7	16	2	Q70Y93_GLAMI	Q70Y93_platostoma
37	22	22.7	17	2	Q9KTQ4_BACHD	Q9KTQ4_bacillus ha
38	22	22.7	18	2	Q7M4O7_HUMAN	Q7M4O7_homo sapien
39	22	22.7	18	2	Q9TWL5_LUCCU	Q9TWL5_lucilia cup
40	22	22.7	18	2	Q9TRB6_PIG	Q9TRB6_sus scrofa
41	22	22.7	18	2	Q3ZSL3_HORVU	Q3ZSL3_hordeum vul
42	22	22.7	18	2	Q70Y99_GLAMI	Q70Y99_bacillus p
43	21.5	22.2	17	1	COG2_CARMA	P81609_carcinus ma
44	21	21.6	9	2	Q30750_BRWAM	Q30750_erwinia amy
45	21	21.6	9	2	Q65711_BEV	Q65711_berne virus

ALIGNMENTS

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RESULT 1
ID 046473_FELCA PRELIMINARY; PRT; 17 AA.
AC 046473;
DT 01-JUN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JUN-1998, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE 07-FEB-2006, entry version 18.
DE Lactase dehydrogenase A (Fragment).
GN Name=LDHA;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC Felinae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=domesticus;
RX MEDLINE=97141918; PubMed=8988168;
RA Lyons L.A., Laughlin T.F., Copeland N.G., Jenkins N.A., Womack J.E.,
RA O'Brien S.J.;
RT "Comparative anchor tagged sequences (CATS) for integrative mapping of
RT mammalian genomes."
RL Nat. Genet. 15:47-56 (1997).
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CC -----
DR EMBL; AF012095; AAC00072.2; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 17
FT NON_TER 17
SO SEQUENCE 17 AA; 2018 MW; E47943B2E187C1FC CRC64;

Query Match 35.1%; Score 34; DB 2; Length 17;
Best Local Similarity 46.2%; Pred. No. 2.6e+02;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GOKATNIPFYTAP 15
   |||:|:|:|
Db 3 GORVNIFKFLIP 15

RESULT 2
Q70Y88_GLAMI PRELIMINARY; PRT; 8 AA.
ID Q70Y88;
AC Q70Y88;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Ribosomal protein (Fragment).
DE Name=Ips16;
OS Platostoma fimbriatum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Eukaryota; Viridiplantae; Magnoliophyta; eudicotyledons; core eudicotyledons;
```

OC asterids; lamids; Lamiales; Lamiaceae; Nepetoideae; Ocimeae;
OC Platanoma.
OC NCBI_TaxID=204168;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15019625; DOI=10.1016/j.jmpev.2003.08.002;
RA Paton A., Springate D.A., Sude S., Otiemo D., Grayer R., Harley M.M.,
RA Willis F., Simonds M.S.J., Powell M.P., Savolainen V.;
RT "Phylogeny and evolution of basil and allies (Ocimeae, Labiales)
RT based on three plastid DNA regions";
RL Mol. Phylogenet. Evol. 31:277-299(2004).
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CC -----
DR EMBL: AJ505368; CAD45489.1; -; Genomic DNA.
DR GO: GO:0003735; F:structural constituent of ribosome; IEA.
KM Ribosomal protein.
FT NON_TER 1
FT TER 8
SQ SEQUENCE 8 AA; 789 MW; 86786772D1BA4772 CRC64;

Query Match 33.0%; Score 32; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 11 PYTAG 16
Db 2 PYTPG 7

RESULT 3
O9TWM4 LUCCU PRELIMINARY; PRT; 18 AA.
AC O9TWM4
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE 25 kDa chymotrypsin-like enzyme (Fragment).
OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Cecidoidea;
OC Calliphoridae; Lucilia.
OX NCBI_TaxID=7375;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=95219141; PubMed=7704304;
RA Casu R.E., Pearson R.D., Jarney J.M., Cadogan L.C., Riding G.A.,
RA Telli R.L.;
RT "Excretory/secretory chymotrypsin from Lucilia cuprina: purification,
RT enzymatic specificity and amino acid sequence deduced from mRNA";
RL Insect Mol. Biol. 3:201-211(1994).
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CC -----
SQ SEQUENCE 18 AA; 1922 MW; 352EB0729B126B11 CRC64;

Query Match 29.4%; Score 28.5; DB 2; Length 18;
Best Local Similarity 58.3%; Pred. No. 2.3e+03;
Matches 7; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

OY 2 DQQRAT-NIPY 12
Db 3 NGQEAIVGQFPY 14

RESULT 4
O8LIY7 PLEBO PRELIMINARY; PRT; 16 AA.
AC O8LIY7
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.

DT 07-FEB-2006, entry version 7.
DE Proteolysis-inducing tag (Fragment).
OS Plectonema boryanum
OC Bacteria; Cyanobacteria; Oscillatoriales; Lepotryngbrya.
OX NCBI_TaxID=1184;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=UTEX 485;
RX MEDLINE=21970088; PubMed=11972342; DOI=10.1093/nar/30.9.2025;
RA Williams K.P.;
RT "Descent of a split RNA";
RL Nucleic Acids Res. 30:2025-2030(2002).
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CC -----
DR EMBL: AY082652; AAM03311.1; -; Genomic DNA.
FT NON_TER 1
FT TER 1
SQ SEQUENCE 16 AA; 1640 MW; 60FE5985B9B00982 CRC64;

Query Match 28.4%; Score 27.5; DB 2; Length 16;
Best Local Similarity 53.8%; Pred. No. 3.1e+03;
Matches 7; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

OY 6 ATNIFPY--TAP 15
Db 1 ANNIVPFARKTAP 13

RESULT 5
O7M4W6 FLAVE PRELIMINARY; PRT; 18 AA.
AC O7M4W6
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DE 07-FEB-2006, entry version 6.
DE Protein P11 (Fragment).
OS Flammulina velutipes.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Agaricales; Tricholomataceae; Flammulina.
OX NCBI_TaxID=38945;
RN [1]
RP PROTEIN SEQUENCE.
RA Sakamoto Y., Ando A., Tamai Y., Miura K.;
RL Submitted (NOV-1999) to the PIR data bank.
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CC -----
DR PIR: A59137; A59137.
FT NON_TER 1
FT TER 1
SQ SEQUENCE 18 AA; 1956 MW; FB0434B0AF005AEC CRC64;

Query Match 27.8%; Score 27; DB 2; Length 18;
Best Local Similarity 80.0%; Pred. No. 4.2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 11 PYTAP 15
Db 2 PYTSP 6

RESULT 6
O7S007 NEUCR PRELIMINARY; PRT; 15 AA.
AC O7S007
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DE 07-FEB-2006, entry version 8.
DE Predicted protein.
GN ORFNames=NCU09752.1;
GN Neurospora crassa.

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OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=74-OR23-1A / FGSC 987;
RX MEDLINE=22598136; PubMed=12712197; DOI=10.1038/nature01554;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehm B.,
RA Elkins T., Engle R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Tanakiev P., Bell-Pedersen D., Nelson M.A.,
RA Werner-Washburne M., Selitrenikoff C.P., Kinsey J.A., Braun E.L.,
RA Zelter A., Schulte U., Kothe G.O., Tedd G., Mewes H.-W., Staben C.,
RA Marcotte E., Greenberg D., Roy A., Foley K., Naylor U.,
RA Stange-Thomann N., Barrett R., Gierke S., Kamal M., Kamyssele M.,
RA Mauceli E., Bielke C., Rudd S., Frisman D., Kryzofova S.,
RA Rasmussen C., Metznerberg R.L., Perkins D.D., Kroken S., Cogoni C.,
RA Marino G., Catchside D.E.A., Li W., Pratt R.J., Omani S.A.,
RA Desouza C.P.C., Glaes N.L., Orbach M.J., Berglund J.A., Voelker R.,
RA Yarden O., Plamann M., Sella S., Dunlap J.C., Radford A., Aramayo R.,
RA Navig D.O., Alex L.A., Mannheim G., Ebole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.W.;
RT "The genome sequence of the filamentous fungus Neurospora crassa.";
RL Nature 422:859-868(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AABX01000580; EAA28619.1; -; Genomic DNA.
SQ SEQUENCE 15 AA; 1832 MW; 012D0180A8C7089D CRC64;

Query March 26.8%; Score 26; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 5.1e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 NIPYT 13
| | | |
Db 2 NVFET 7

RESULT 7
Q7M198 STRFR PRELIMINARY; PRT; 18 AA.
AC Q7M198
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE 24k serine proteinase (EC 3.4.21.-) (Fragment).
OS Streptomyces fradiae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycetaceae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=1906;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=92155439; PubMed=1786859; DOI=10.1016/0020-711X(91)90133-8;
RA Silha U., Woltz S.A., Lad P.J.;
RT "Two new extracellular serine proteases from Streptomyces fradiae.";
RL Int. J. Biochem. 23:979-984(1991).
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CC -----
DR PIR; A61577; A61577.
FT NON_TER 1
FT TER 18
SQ SEQUENCE 18 AA; 2004 MW; 6D6DA167845934A5 CRC64;

Query March 26.8%; Score 26; DB 2; Length 18;
Best Local Similarity 41.7%; Pred. No. 6.2e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

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QY 1 VDQKATNIPY 12
| | | | |
Db 2 VGTTRAQGFPPW 13

RESULT 8
CWP16_LYCES STANDARD; PRT; 15 AA.
ID CWP16_LYCES
AC P80812;
DT 25-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DT 25-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE 40 kDa cell wall protein (Fragment).
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
OX NCBI_TaxID=4081;
RN [1]
RP PROTEIN SEQUENCE AND SUBCELLULAR LOCATION.
RX MEDLINE=97332671; PubMed=918482; DOI=10.1074/jbc.272.25.15841;
RA Robertson D., Mitchell G.P., Gilroy J.G., Gerrish C., Bolwell G.P.,
RA Slabas A.R.;
RT "Differential extraction and protein sequencing reveals major
RT differences in patterns of primary cell wall proteins from plants.";
RL J. Biol. Chem. 272:15841-15846(1997).
CC -!- SUBCELLULAR LOCATION: Cell wall.
CC -----
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CC -----
DR Cell wall; Direct protein sequencing.
KW Cell wall; Direct protein sequencing.
FT CHAIN 1
FT 1 >15
FT /FTID=PRO_0000079677.
SQ SEQUENCE 15 AA; 1705 MW; 1F328E5C82CA77BE CRC64;

Query March 25.8%; Score 25; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 7.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 FPYT 13
| | | | |
Db 6 FPYT 9

RESULT 9
O9UR63_EMENT PRELIMINARY; PRT; 15 AA.
ID O9UR63_EMENT
AC O9UR63;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Beta-D-FRUCTOFURANOSIDE FRUCTOHYDROLASE 60 kDa high molecular weight
DE isoform (EC 3.2.1.26) (Fragment).
DE Emeritella nidulans (Aspergillus nidulans).
OS Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiaceae; Trichocomaceae; Emeritella.
OX NCBI_TaxID=162425;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=96409246; PubMed=8814228; DOI=10.1016/0167-4838(96)00073-8;
RA Chen J.S., Saxton J., Hemming F.W., Peberdy D.F.;
RT "Purification and partial characterization of the high and low
RT molecular weight form (S- and F-form) of invertase secreted by
RT Aspergillus nidulans.";
RL Biochim. Biophys. Acta 1296:207-218(1996).
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CC -----
DR GO; GO:0004564; F-beta-fructofuranosidase activity; IEA.

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SQ SEQUENCE 15 AA; 1588 MW; 2C992B42211366BB CRC64;
Query Match 25.8%; Score 25; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 7.6e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 PYTAP 15
DB 10 PYTEP 14

RESULT 10
Q3ZEV4_9CHAR PRELIMINARY; PRT; 16 AA.
AC Q3ZEV4_7
DT 27-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 27-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE ATP synthase F0 subunit 8 (Fragment).
GN Name=ATP8;
OS Tringa totanus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archoeoptera; Aves; Neognathae; Charadriiformes; Scolopacidae; Tringa.
OX NCBI_TaxID=171271;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Pereira S.L., Baker A.J.;
RT "Multiple gene evidence for parallel evolution and retention of
RT ancestral morphological states in the shanks (Charadriiformes:
RT Scolopacidae).";
RL Condor 107:514-526 (2005).
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CC -----
CC EMBL; AY894271; AAX94014.1; -; Genomic DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1965 MW; 75D680373ACCF82D CRC64;
Query Match 25.8%; Score 25; DB 2; Length 16;
Best Local Similarity 55.6%; Pred. No. 8.2e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 TNIPFYTAP 15
DB 6 TKIRPTWTP 14

RESULT 11
Q71AT5_9CRYP PRELIMINARY; PRT; 14 AA.
AC Q71AT5;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE tmRNA proteolysis tag (Fragment).
GN Name=ssrA;
OS Rhodomonas salina.
OG Plastid.
OC Eukaryota; Cryptophyta; Cryptomonadaceae; Rhodomonas.
OX NCBI_TaxID=52970;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=CCMP1319;
RX PubMed=14681369; DOI=10.1093/nar/gkh102;
RA Gueneau de Novoa P., Williams K.P.;
RT "The tmRNA website: reductive evolution of tmRNA in plastids and other
RT endosymbionts.";
RL Nucleic Acids Res. 32:D104-D108 (2004).
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CC -----
DR EMBL; AF550355; AAQ12671.1; -; Genomic DNA.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1528 MW; D995F9B3698210B9 CRC64;
Query Match 24.7%; Score 24; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 1e+04;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 ATNIFYPT 13
DB 1 ANNTVPS 8

RESULT 12
Q7TPH9_PHOSU PRELIMINARY; PRT; 16 AA.
AC Q7TPH9;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Per2 protein (Fragment).
GN Name=Per2;
OS Phodopus sungorus (Striped hairy-footed hamster) (Djunganian hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Cricetidae; Cricetinae; Phodopus.
OX NCBI_TaxID=10044;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Souza V., Semikhodskii A.G., London A.S.I.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AY316536; AAP87362.1; -; mRNA.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1831 MW; 845CE49E44AE531 CRC64;
Query Match 24.7%; Score 24; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 1.2e+04;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 11 PYTAPGKQ 18
DB 6 PLTSPRKE 13

RESULT 13
Q3ZEV6_9CHAR PRELIMINARY; PRT; 16 AA.
AC Q3ZEV6;
DT 27-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 27-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE ATP synthase F0 subunit 8 (Fragment).
GN Name=ATP8;
OS Tringa flavipes.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archoeoptera; Aves; Neognathae; Charadriiformes; Scolopacidae; Tringa.
OX NCBI_TaxID=161739;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Pereira S.L., Baker A.J.;
RT "Multiple gene evidence for parallel evolution and retention of
RT ancestral morphological states in the shanks (Charadriiformes:
RT Scolopacidae).";
RL Condor 107:514-526 (2005).
CC -----
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 CC EMBL: AY894261; AAX93984.1; -; Genomic_DNA.
 DR GO: 0005739; C:mitochondrion; IEA.
 DR Mitochondrion.
 FT NON_TER 1
 SQ SEQUENCE 16 AA; 1893 MW; 6FF802724F1F82D CRC64;
 Query Match 24.7%; Score 24; DB 2; Length 16;
 Best Local Similarity 50.0%; Pred. No. 1.2e+04;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 Oy 6 ATNIPYAP 15
 Db 5 ATKTPWTWP 14
 RESULT 14
 Q65YZ6 HORSE PRELIMINARY; PRT; 17 AA.
 ID Q65YZ6 HORSE PRELIMINARY; PRT; 17 AA.
 AC Q65YZ6;
 DT 25-OCT-2004, integrated into UniProtKB/TrEMBL.
 DT 25-OCT-2004, sequence version 1.
 DT 07-FEB-2006, entry version 6.
 DE Asparagine-linked glycosylation 8 homolog (Fragment).
 GN Name=ALG8;
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hasegawa T., Sato F., Tozaki T., Hirota K.;
 RT "Fine mapping of equine chromosomes corresponding to HSA11";
 RL Submitted (MAR-2004) to the EMBL/Genbank/DBJ databases.
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 CC EMBL: AB16785; BAD44704.1; -; Genomic_DNA.
 DR SML: Q65YZ6; 1-72.
 DR SML: Q65YZ6; BAD44704.1; -; Genomic_DNA.
 FT NON_TER 1
 SQ SEQUENCE 17 AA; 1907 MW; 24AB4757508FF8FC CRC64;
 Query Match 24.7%; Score 24; DB 2; Length 17;
 Best Local Similarity 50.0%; Pred. No. 1.3e+04;
 Matches 5; Conservative 3; Mismatches 0; Indels 2; Gaps 1;
 Oy 8 NIFP-YTAP 15
 Db 6 SLFPLFLFTAP 15
 RESULT 15
 Q3TW38 MOUSE PRELIMINARY; PRT; 18 AA.
 ID Q3TW38 MOUSE PRELIMINARY; PRT; 18 AA.
 AC Q3TW38;
 DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2006, entry version 1.
 DE Osteoclast-like cell cDNA, RIKEN full-length enriched library,
 DE clone:1420034D23 product:RNA binding motif, single stranded
 DE interacting protein 1, full insert sequence. (Fragment).
 GN Name=Rhms1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=C57BL/6J;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning";
 RL Methods Enzymol. 303:19-44(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J;
 RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
 Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
 Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
 Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
 Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
 Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
 Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
 Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
 di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
 Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
 Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
 Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
 Hill D., Hummelbeck L., Iacono M., Ikeo K., Iwama A., Ishikawa H.,
 Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
 Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
 Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
 Linuati S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
 Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
 Mottagui-Tabar S., Mulder N., Nakano N., Nakamura H., Ng P.,
 Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
 Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,
 Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
 Roest B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
 Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
 Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
 Sperling S., Stupka E., Sugita K., Sultana R., Takenaka Y., Taki K.,
 Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
 Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yang K.,
 Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
 Gilmord S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
 Wahlestedt C., Watnick J.S., Hume D.A., Kai C., Sasaki D., Tomaru U.,
 Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
 Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashita N.,
 Kawashima T., Kojima M., Kondo S., Kono H., Nakano K., Nimomiya N.,
 Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
 Tagami M., Waki K., Watanabe A., Okamura-Oho Y., Suzuki H., Kawai J.,
 Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome";
 RL Science 309:1559-1563(2005).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J;
 RX PubMed=16141073; DOI=10.1126/science.1112009;
 RG RIKEN Genome Exploration Research Group, and Genome Science Group
 RG (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense Transcription in the Mammalian Transcriptome";
 RL Science 309:1564-1566(2005).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 Yagi K., Tomaru U., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 Schirini L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 Blake J.A., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
 Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 Grimmer S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
 Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 Maglott D.R., Matsuda L., Marchionni L., McKenzie L., Miki H.,
 Nagashima T., Numata K., Okido T., Pavan W.J., Pesole G.,

RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sander A., Schneider C., Sempke C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita K.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Borle A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carinci P., Hayatsu N.,
RA Hironaka-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Maki K., Kawai J., Aizawa K., Atakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yaunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
[5]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Atakawa T., Hara A., Fukunishi Y., Konno H., Adachi U., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schirni L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carinci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guenrich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombere P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshaw-Borle A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[6]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
[7]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama Y., Nishi K., Katsunai T., Tashiro H., Itoh M.,
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
[8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;
RX Atakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watanaki A.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.

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CC -----
DR EMBL: AK159851; BAE35428.1; -; mRNA.
DR MGI: MGI:1861774; Rbm31.
DR GO: GO:0005634; C:nucleus; RCA.
DR GO: GO:0003690; C:nucleus; RCA.
DR GO: GO:0003723; F:RNA binding; RCA.
DR GO: GO:0003657; F:single-stranded DNA binding; RCA.
DR GO: GO:0006260; P:DNA replication; RCA.
FT NON TER 1 1
SQ SEQUENCE 18 AA; 2003 MW; 82F0AB5FD94EBA14 CRC64;
Query Match 24.7%; Score 24; DB 2; Length 18;
Best Local Similarity 80.0%; Pred. No. 1.4e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 11 PYTP 15
DB 11 PYTP 15
Search completed: May 30, 2006, 15:07:41
Job time : 69.6667 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 30, 2006, 14:59:31 ; Search time 61.6667 Seconds
(without alignments)
133.458 Million cell updates/sec

Title: US-10-758-165A-10
Perfect score: 97
Sequence: 1 VDCQKATNIPPTATGKQ 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 902922

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	97	100.0	18	ADRI0610	Adt10610 Cat IGE e
2	87	89.7	18	ADRI0609	Adt10609 Dog IGE e
3	55	56.7	18	ADRI0612	Adt10612 Sheep IGE
4	37	38.1	15	ADCS6890	Adcs6890 Peptide f
5	35	36.1	18	ADRI0611	Adt10611 Horse IGE
6	34	35.1	15	ADCS6890	Adcs6890 Peptide f
7	33.5	34.5	15	ADJ38597	Adj38597 HSV-4 G1Y
8	32.5	33.5	15	ADJ38596	Adj38596 HSV-4 G1Y
9	32.5	33.5	15	ADW78189	Adw78189 Human met
10	32	33.0	9	AAU76520	Aau76520 Anti-Inte
11	32	33.0	9	AAE15818	Aae15818 Human mab
12	32	33.0	9	AEF76312	Aef76312 Prostate
13	32	33.0	11	ADT40399	Adt40399 hSARS vir
14	32	33.0	11	ADST79816	Adst79816 SARS viru
15	32	33.0	11	ADT37929	Adt37929 hSARS vir
16	32	33.0	15	AAV65747	Aav65747 Breast ca
17	32	33.0	15	ABU78631	Abu78631 Novel pro
18	32	33.0	15	ABU78640	Abu78640 Novel pro
19	32	33.0	15	ADN64911	Adn64911 HLA bindi
20	31	32.0	11	AAE02349	Aae02349 Caenorhab
21	31	32.0	12	AAK90344	Aak90344 Macrophag
22	31	32.0	13	ADBJ37003	Adbj37003 Stainless
23	31	32.0	14	AAV31329	Aav31329 B. subtil

24	31	32.0	15	8	ADN64927	Adn64927 HLA bindi
25	31	32.0	15	9	ADM77897	Adm77897 Human can
26	30	30.9	9	6	ABU19961	Abu19961 MHC bindi
27	30	30.9	9	7	ADD94584	Add94584 Human SIM
28	30	30.9	10	7	ADD94544	Add94544 Human SIM
29	30	30.9	11	9	ABE17405	Abe17405 Type II p
30	30	30.9	12	2	AAK49911	Aak49911 Glutamin
31	30	30.9	13	2	AAK49912	Aak49912 Glutamin
32	30	30.9	13	2	AAK49913	Aak49913 Glutamin
33	30	30.9	14	2	AAK49914	Aak49914 Glutamin
34	30	30.9	14	3	AAK39162	Aak39162 Human sec
35	30	30.9	14	3	AAK39163	Aak39163 Human sec
36	30	30.9	15	2	AAK65210	Aak65210 Murine st
37	30	30.9	15	9	ADU70842	Adu70842 Human hep
38	30	30.9	16	2	AAK53562	Aak53562 Birch pol
39	30	30.9	16	8	ADQ90450	Adq90450 RANTES re
40	30	30.9	17	2	AAK95159	Aak95159 bcl-x(L)/
41	30	30.9	18	9	ADV22975	Adv22975 HCV H77 i
42	29	29.9	9	2	AAW24775	Aaw24775 Human imm
43	29	29.9	9	2	AAW80144	Aaw80144 Light cha
44	29	29.9	9	2	AAW80142	Aaw80142 Light cha
45	29	29.9	9	2	AAV40427	Aav40427 Amino aci

ALIGNMENTS

RESULT 1
ID ADR10610 standard; peptide; 18 AA.
XX
AC ADR10610;
XX
DT 21-OCT-2004 (first entry)
XX
DE Cat IGE epitope recognised by monoclonal antibody 3.76, SEQ ID 10.
XX
KM Antiasthmatic; Antiasthmatic; Immunosuppressive; IGE; dog; asthma;
KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
cat.
XX
OS Fells catus.
XX
PN WO2004065936-A2.
XX
PD 05-AUG-2004.
XX
PF 15-JAN-2004; 2004WO-US003566.
XX
PR 16-JAN-2003; 2003US-0440472P.
XX
PA (UYNC-) UNIV NORTH CAROLINA STATE.
XX
PI Hammerberg B;
XX
DR WPI; 2004-593545/57.
XX
PT Novel antibody that specifically binds to mammalian IGE epitope, useful
PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE
PT or treating asthma or anaphylactic shock.
XX
PS Example 6; Page 9; 14pp: English.
XX
CC The present invention relates to a novel monoclonal antibody (I) that
CC specifically binds to a mammalian IGE epitope, where the epitope is
CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
CC (I) is useful for testing an allergen reactivity of an IGE sample. The
CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
CC and corn allergens. The sample is a biological sample collected from a
CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
CC antibodies recognise epitopes on canine IGE corresponding to amino acid
CC residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the

CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with
 CC either pig or human epsilon-chains of IGE. The present sequence is the
 CC cat IGE 3.76 recognition site.
 XX

SO Sequence 18 AA;

Query Match 100.0%; Score 97; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 5,7e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VDGGKATNIFPYTAPGKQ 18
 |||||
 DB 1 VDGGKATNIFPYTAPGKQ 18

RESULT 2

ADRI0609
 ID ADRI0609 standard; peptide; 18 AA.

XX
 AC ADRI0609;

DT 21-OCT-2004 (first entry)

XX Dog IGE epitope recognised by monoclonal antibody 3.76, SEQ ID 9.

XX Antiaesthetic; Antiallergic; Immunosuppressive; IGE; dog; asthma;

KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody.

XX Canis familiaris.

XX WO2004065936-A2.

PN 05-AUG-2004.

XX 15-JAN-2004; 2004WO-US003566.

PR 16-JAN-2003; 2003US-0440472P.

XX (UYN-) UNIV NORTH CAROLINA STATE.

PA Hammerberg B;

XX WPI; 2004-593545/57.

XX Novel antibody that specifically binds to mammalian IGE epitope, useful
 PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE
 PT or treating asthma or anaphylactic shock.

XX Example 6; Page 9; 14pp; English.

PS The present invention relates to a novel monoclonal antibody (I) that

CC specifically binds to a mammalian IGE epitope, where the epitope is

CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.

CC (I) is useful for testing an allergen reactivity of an IGE sample. The

CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut

CC and corn allergens. The sample is a biological sample collected from a

CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for

CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal

CC antibodies recognise epitopes on canine IGE corresponding to amino acid

CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the

CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from

CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and

CC 3.76 were observed to have good cross-reactivity with the epsilon-chain

CC of IGE from cat and horse, but did not exhibit cross-reactivity with

CC either pig or human epsilon-chains of IGE.
 XX
 SO Sequence 18 AA;

Query Match 89.7%; Score 87; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 2,7e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VDGGKATNIFPYTAPG 16
 |||||
 DB 1 VDGGKATNIFPYTAPG 16

RESULT 3

ADRI0612
 ID ADRI0612 standard; peptide; 18 AA.

XX
 AC ADRI0612;

DT 21-OCT-2004 (first entry)

XX Sheep IGE epitope recognised by monoclonal antibody 3.76, SEQ ID 12.

XX Antiaesthetic; Antiallergic; Immunosuppressive; IGE; dog; asthma;

KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;

XX sheep.

XX Ovis aries.

XX WO2004065936-A2.

XX 05-AUG-2004.

XX 15-JAN-2004; 2004WO-US003566.

PR 16-JAN-2003; 2003US-0440472P.

XX (UYN-) UNIV NORTH CAROLINA STATE.

PA Hammerberg B;

XX WPI; 2004-593545/57.

XX Novel antibody that specifically binds to mammalian IGE epitope, useful
 PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE
 PT or treating asthma or anaphylactic shock.

XX Example 6; Page 9; 14pp; English.

XX The present invention relates to a novel monoclonal antibody (I) that

CC specifically binds to a mammalian IGE epitope, where the epitope is

CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.

CC (I) is useful for testing an allergen reactivity of an IGE sample. The

CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut

CC and corn allergens. The sample is a biological sample collected from a

CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for

CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal

CC antibodies recognise epitopes on canine IGE corresponding to amino acid

CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the

CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from

CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and

CC 3.76 were observed to have good cross-reactivity with the epsilon-chain

CC of IGE from cat and horse, but did not exhibit cross-reactivity with

CC either pig or human epsilon-chains of IGE. The present sequence is the
 XX
 SO Sequence 18 AA;

Query Match 56.7%; Score 55; DB 8; Length 18;
 Best Local Similarity 66.7%; Pred. No. 0.067;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 VDGGKATNIFPYTAP 15
 |||||
 DB 1 VDGGEDRNLFPSYTAP 15

RESULT 4
 ADC56890

```

ID ADC56890 standard; peptide: 15 AA.
XX
AC ADC56890;
XX
DT 18-DEC-2003 (first entry)
XX
DE Peptide fragment Seq ID7 related to human protein 36-41.
XX
KW human; protein 36-41; arrhythmia; asthma; dementia.
XX
OS Homo sapiens.
XX
PN CN1382718-A.
XX
PD 04-DEC-2002.
XX
PF 26-APR-2001; 2001CN-00112751.
XX
PR 26-APR-2001; 2001CN-00112751.
XX
PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
PI WPI; 2003-269480/27.
XX
DR New human macroprotein-36-41, encoding polynucleotide, antagonist and
XX PT recombinant production, useful for treating dementia, arrhythmia, asthma
XX PT and digestive ulcers.
XX
PS Example 6; SEQ ID NO 7; 33pp; Chinese.
XX
CC This invention relates to a novel protein, human protein 36-41, and the
XX CC DNA sequence encoding it. The protein of the invention may be useful for
XX CC the treatment of diseases such as arrhythmia, asthma and dementia. The
XX CC present sequence is the amino acid sequence of a peptide fragment of
XX CC human protein 36-41 which was used in the exemplification of the
XX CC invention.
XX
SQ Sequence 15 AA;

Query Match 38.1%; Score 37; DB 7; Length 15;
Best Local Similarity 40.0%; Pred. No. 59;
Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 VDGQKATNIPPYTAP 15
   :||: |||: ||
Db 1 MDGKMQPNSFPWQSP 15

RESULT 5
ADRI0611
ID ADRI0611 standard; peptide: 18 AA.
XX
AC ADRI0611;
XX
DT 21-OCT-2004 (first entry)
XX
DE Horse IGE epitope recognised by monoclonal antibody 3.76, SEQ ID 11.
XX
KW Antiasthmatic; Anti allergic; Immunosuppressive; IGE; dog; asthma;
XX KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
XX KW horse.
XX
OS Equus caballus.
XX
PN WO2004065936-A2.
XX
PD 05-AUG-2004.
XX
PF 15-JAN-2004; 2004WO-US003566.
XX
PR 16-JAN-2003; 2003US-0440472P.

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XX
PA (UNNC-) UNIV NORTH CAROLINA STATE.
XX
PI Hammerberg B;
XX
PI WPI; 2004-593545/57.
XX
DR Novel antibody that specifically binds to mammalian IGE epitope, useful
XX PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE
XX PT or treating asthma or anaphylactic shock.
XX
PS Example 6; Page 9; 14pp; English.
XX
CC The present invention relates to a novel monoclonal antibody (I) that
XX CC specifically binds to a mammalian IGE epitope, where the epitope is
XX CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
XX CC (I) is useful for testing an allergen reactivity of an IGE sample. The
XX CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
XX CC and corn allergens. The sample is a biological sample collected from a
XX CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
XX CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
XX CC antibodies recognise epitopes on canine IGE corresponding to amino acid
XX CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the
XX CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from
XX CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
XX CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
XX CC of IGE from cat and horse, but did not exhibit cross-reactivity with
XX CC either pig or human epsilon-chains of IGE. The present sequence is the
XX CC horse IGE 3.76 recognition site.
XX
SQ Sequence 18 AA;

Query Match 36.1%; Score 35; DB 8; Length 18;
Best Local Similarity 44.4%; Pred. No. 1.66+02;
Matches 8; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

QY 1 VDGQKATNIPPYTAPGKQ 18
   :||| ||| ||
Db 1 IDGQRVDEQFPQHGIVKQ 18

RESULT 6
ADC64569
ID ADC64569 standard; peptide: 15 AA.
XX
AC ADC64569;
XX
DT 18-DEC-2003 (first entry)
XX
DE Horse immunoglobulin E, IGE, heavy chain immunogenic peptide P5.
XX
KW Horse; immunoglobulin E; IGE; heavy chain; immunogen; allergy.
XX
OS Equus caballus.
XX
PN US2003087314-A1.
XX
PD 08-MAY-2003.
XX
PF 08-NOV-2001; 2001US-00052788.
XX
PR 08-NOV-2001; 2001US-00052788.
XX
PA (REGC ) UNIV CALIFORNIA.
XX
PI Gershwin LJ, Pettigrew HD, Kalina WV;
XX
PI WPI; 2003-765437/72.
XX
CC Immunogenic composition comprising an isolated equine immunoglobulin E
XX PT polypeptide that induces production of antibodies which specifically bind
XX PT to equine immunoglobulin E.

```

PS Example 1; Page 8; 14pp; English.

XX The invention relates to an immunogenic composition comprising an
CC isolated polypeptide having an amino acid sequence that is at least 80%
CC identical to 6 (SI-56), 15 amino acid peptide sequences derived from
CC equine immunoglobulin E (the composition induces production of an
CC antibody that specifically binds to equine immunoglobulin (Ig)E, the six
CC polypeptides are not explicitly identified in the specification. Also
CC included are a composition comprising an antibody that specifically binds
CC to a polypeptide at least 80% identical to (SI)-(56), an antibody that
CC specifically binds to equine IgE made by the process of immunising an
CC animal with a polypeptide at least 80% identical to (SI)-(56), making an
CC antibody that specifically binds to equine IgE (involving immunising an
CC animal with a composition further comprising an isolated polypeptide (the
CC amino acid sequence of the polypeptide is at least 80% identical to (SI)-
CC (56)), and collecting antiserum from the animal) and a kit for detection
CC of equine IgE in a biological sample comprising the antibody and means
CC for detecting specific binding of the antibody to equine IgE. The
CC antibody is useful for detecting equine IgE protein in a biological
CC sample (serum) which involves contacting the sample with the antibody,
CC thus forming an antigen/antibody complex, and detecting the presence or
CC absence of the antigen/antibody complex. The antibody and antigen are
CC immobilised on a solid surface. The antibody is labelled such that the
CC complex can be detected. The complex is detected using a second labelled
CC antibody. The peptides are useful for generating antibodies specific for
CC IgE which can serve as a diagnostic test for allergy. The present
CC sequence is a horse immunoglobulin E, IgE, heavy chain immunogenic
CC peptide from the middle portion of the C2 region.

XX Sequence 15 AA;

Query Match 35.1%; Score 34; DB 7; Length 15;
Best Local Similarity 54.5%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 VDGQKATNIFP 11
: |||||
Db 2 IDGQKVDQGF 12

RESULT 7
ADJ38597
ID ADJ38597 standard; peptide; 15 AA.

XX AC ADJ38597;

XX DT 06-MAY-2004 (first entry)

XX DE HSV-4 Glycoprotein B late domain motif mutant peptide #1.

XX KM Virucide; HSV infection; antiviral; late domain motif; mutein; mutant.

XX OS Human herpesvirus 4.

XX OS Synthetic.

XX FT Key Location/Qualifiers

FT Misc-difference 6 /note= "Wild-type residue replaced with Ala"

XX PN WO2004009027-A2.

XX PD 29-JAN-2004.

XX PF 21-JUL-2003; 2003WO-US022828.

XX PR 19-JUL-2002; 2002US-0397265P.

XX PR 19-JUL-2002; 2002US-0397477P.

XX PR 03-MAR-2003; 2003US-0451903P.

XX PA (MYRI-) MYRIAD GENETICS INC.

XX PI Morham S, Zavitz K, Hobden A;

XX WPI; 2004-123282/12.

XX Use of cells displaying herpes simplex virus (HSV) altered budding
PT phenotype for the manufacture of a medicament for treating HSV infection.

XX Example 13; Page 66; 74pp; English.

XX The present invention relates to cells displaying herpes simplex virus
CC (HSV) altered budding phenotype which are useful for the manufacture of a
CC medicament for treating HSV infection. The medicament further comprises
CC an adjuvant capable of stimulating cellular immune response e.g. IL-2, IL
CC -4, IL-12, IL-18 or gamma-interferon. The cells are human cells and
CC contain a nucleic acid encoding a mutant HSV protein or a nucleic acid
CC encoding the polypeptide sufficient for virus-like particle assembly but
CC devoid of late-domain motifs. The nucleic acid is within an HSV genome.
CC The genome is devoid of late domain motifs capable of effecting viral
CC budding. The composition also comprises a compound capable of interfering
CC with the protein-protein interaction between a host cell protein capable
CC of binding a late domain motif and a HSV protein containing a late domain
CC motif. The composition further comprises another HSV protein or its
CC immunogenic fragment, and/or a nucleic acid encoding the other HSV
CC protein or the immunogenic fragment. The present sequence is a mutant HSV
CC peptide, derived from the wild-type peptide ADJ38596, used to illustrate
CC the invention.

XX Sequence 15 AA;

Query Match 34.5%; Score 33.5; DB 8; Length 15;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 6 ATNIFPYTAPGK 17
|||: |||||
Db 1 ATTV-PATAPGK 11

RESULT 8
ADJ38596
ID ADJ38596 standard; peptide; 15 AA.

XX AC ADJ38596;

XX DT 06-MAY-2004 (first entry)

XX DE HSV-4 Glycoprotein B late domain motif wild-type peptide.

XX KM Virucide; HSV infection; antiviral; late domain motif.

XX OS Human herpesvirus 4.

XX PN WO2004009027-A2.

XX PD 29-JAN-2004.

XX PF 21-JUL-2003; 2003WO-US022828.

XX PR 19-JUL-2002; 2002US-0397265P.

XX PR 19-JUL-2002; 2002US-0397477P.

XX PR 03-MAR-2003; 2003US-0451903P.

XX PA (MYRI-) MYRIAD GENETICS INC.

XX PI Morham S, Zavitz K, Hobden A;

XX WPI; 2004-123282/12.

XX Use of cells displaying herpes simplex virus (HSV) altered budding
PT phenotype for the manufacture of a medicament for treating HSV infection.

XX Example 13; Page 66; 74pp; English.

CC The present invention relates to cells displaying herpes simplex virus
CC (HSV) altered budding phenotype which are useful for the manufacture of a
CC medicament for treating HSV infection. The medicament further comprises
CC an adjuvant capable of stimulating cellular immune response e.g. IL-2, IL
CC -4, IL-12, IL-18 or gamma-interferon. The cells are human cells and
CC contain a nucleic acid encoding a mutant HSV protein or a nucleic acid
CC encoding the polypeptide sufficient for virus-like particle assembly but
CC devoid of late-domain motifs. The nucleic acid is within an HSV genome.
CC The genome is devoid of late domain motifs capable of effecting viral
CC budding. The composition also comprises a compound capable of interfering
CC with the protein-protein interaction between a host cell protein capable
CC of binding a late domain motif and a HSV protein containing a late domain
CC motif. The composition further comprises another HSV protein or its
CC immunogenic fragment, and/or a nucleic acid encoding the other HSV
CC protein or the immunogenic fragment. The present sequence is a wild-type
CC HSV peptide, from which mutant sequences (ADJ38597-ADJ38600) were
CC generated for use in the invention.

SO Sequence 15 AA;

Query Match 33.5%; Score 32.5; DB 8; Length 15;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 6 ATNIFPYTPAGK 17
||:|||||
DB 1 ATTV-PTTPAGK 11

RESULT 9
ADM78189
ID ADM78189 standard; peptide; 15 AA.

AC ADM78189;

DT 07-APR-2005 (first entry)

DE Human metabolic therapy target peptide PACT.

XX DEF domain; MAP kinase; cytosolic; cardiovascular-gen.; cardiac;
XX vasoactive; hypotensive; antiarteriosclerotic; antiinflammatory;
XX antiallergic; immunosuppressive; antibacterial; antiaesthetic;
XX dermatological; antidiabetic; gastrointestinal-gen.; antitumor;
XX thrombolytic; neuroprotective; ophthalmological; antianemic;
XX antipyretic; uropathic; antiparasitic; hepatotropic; antianemic;
XX muscular-gen.; thyromimetic; antithyroid; gynecological; nephrotropic;
XX hepatotropic; virucide; anti-HIV; anabolic; hypertensive; anorectic;
XX endocrine-gen.; neuroleptic; nootropic; antiparkinsonian; anticonvulsant;
XX antidepressant; antidiabetic; sedative; hypnotic; CNS-gen.;
XX antifertility; cancer; cardiovascular disease; inflammation;
XX metabolic disorder; neuropathy; sleep disorder.

KW Homo sapiens.

OS WO200507090-A2.

PN 27-JAN-2005.

PD 02-JUL-2004; 2004WO-US021514.

PF 03-JUL-2003; 2003US-0484761P.

PR (HARD) HARVARD COLLEGE.

PA Blenis J, Murphy LO;

XX WPI, 2005-112720/12.

FT Identification of compound for treating e.g. cancer by culturing cells
PT expressing target protein in the presence of growth factor, cytokine,
PT tumor promoter or oncogene and assessing binding after contacting with
XX the compound.

PS Claim 14; Page 64; 104pp; English.

XX The invention relates to a novel method for the identification of a
CC therapeutic compound. The method involves providing test cells that
CC express a target protein containing a DEF domain and MAP kinase;
CC culturing the cells in the presence of growth factor, cytokine, tumor
CC promoter or oncogene; contacting the cells with a candidate compound; and
CC assessing the binding of the MAP kinase to the DEF domain relative to the
CC binding in the absence of the candidate compound. The invention further
CC comprises a method for the identification of a therapeutic compound; a
CC method for treatment of cancer, which involves administering a target
CC protein; and an antibody that specifically binds to phospho-T-325 c-Fos
CC (preferably polyclonal or monoclonal). The novel therapeutic compounds
CC have the following activities: cytosolic; cardiovascular-gen.; cardiac;
CC vasoactive; hypotensive; antiarteriosclerotic; antiinflammatory;
CC antiallergic; immunosuppressive; antibacterial; antiaesthetic;
CC dermatological; antidiabetic; gastrointestinal-gen.; antitumor;
CC thrombolytic; neuroprotective; ophthalmological; antianemic;
CC antipyretic; uropathic; antiparasitic; hepatotropic; antianemic; muscular
CC -gen.; thyromimetic; antithyroid; gynecological; nephrotropic;
CC hepatotropic; virucide; anti-HIV; anabolic; hypertensive; anorectic;
CC endocrine-gen.; neuroleptic; nootropic; antiparkinsonian; anticonvulsant;
CC antidepressant; antidiabetic; sedative; hypnotic; CNS-gen.; and
CC antifertility. The therapeutic compound may be used in the treatment
CC of: cancer; cardiovascular disorders; inflammatory disorders; metabolic
CC disorders; neuropathy or a behavioural disorder; and a sleep disorder.
CC This sequence represents a metabolic therapy target peptide of the
CC invention.

SO Sequence 15 AA;

Query Match 33.5%; Score 32.5; DB 9; Length 15;
Best Local Similarity 66.7%; Pred. No. 3.4e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 5 KATNIFPYTPAG 16
||| |||||
DB 1 KAT--PYTPPG 9

RESULT 10
AAU76520
ID AAU76520 standard; peptide; 9 AA.

AC AAU76520;

DT 05-JUN-2002 (first entry)

DE Anti-Interleukin-12 (IL-12) antibody CDR3 light chain.

XX Human; antibody; anti-interleukin-12; CDR; light chain; circulatory;
XX complementarity determining region; neuroprotective; antiparasitic;
XX immunostimulant; cytosolic; anti-microbial; porphyrin; infection;
XX multiple sclerosis; immune disorder; cardiovascular; malignant disease;
XX neurological disorder.

KW Homo sapiens.

OS WO200212500-A2.

PN 14-FEB-2002.

PD 07-AUG-2001; 2001WO-US024720.

PF 07-AUG-2000; 2000US-0223358P.

PR 29-SEP-2000; 2000US-0236827P.

PR 01-AUG-2001; 2001US-00920262.

PA (CENZ) CENTOCOR INC.
XX Giles-Komar J, Knight DM, Perlett D, Scallion B, Shealy D;
XX

DR WPI: 2002-257482/30.

XX New mammalian anti-IL-12 antibodies, useful for diagnosing or treating IL

PT -12 related conditions, e.g. psoriasis or multiple sclerosis, as well as

PT other for treating immune, infectious, malignant or neurological

PT disorders.

XX

XX Claim 41; Page 93; 96pp; English.

XX

XX The invention relates to novel isolated mammalian anti-interleukin-12 (IL

CC -12) antibodies. The antibodies comprise at least one complementarily

CC determining region (CDR) of a heavy or light chain, a heavy chain or

CC light chain variable region, or a heavy chain or light chain constant

CC region. The anti-IL-12 antibodies are useful in methods for diagnosing or

CC treating IL-12 related conditions, e.g. psoriasis or multiple sclerosis.

CC The antibodies are also useful for treating immune, cardiovascular,

CC infectious, malignant or neurological disorders or diseases. The present

CC sequence represents the amino acid sequence of human anti-interleukin-12

CC (IL-12) antibody CDR3 light chain

XX

SO Sequence 9 AA:

Query Match 33.0%; Score 32; DB 5; Length 9;

Best Local Similarity 83.3%; Pred. No. 2.1e+06;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 8 NIPYPT 13

DB 4 NIPYPT 9

RESULT 11

AAE15818

ID AAE15818 standard; peptide; 9 AA.

XX

AC AAE15818;

XX

DT 26-MAR-2002 (first entry)

XX

DE Human mAb 12B1 VK complementarity determining region (CDR) #3.

XX

XX Human; sialoadhesin factor-3; SAF-3; therapy; cancer; inflammation;

XX autoimmunity; allergy; asthma; infection; central nervous system; CNS;

XX rheumatoid arthritis; multiple sclerosis; stem cell mobilisation; AIDS;

XX haematopoietic development; anaemia; chemoprotective agent; cytotoxic;

XX immunoglobulin; complementarity determining region; CDR; protozoacide;

XX antiinflammatory; immunosuppressive; anti-HIV; antibacterial; virucide;

XX fungicide; neuroprotective; light chain variable region; VK; mAb;

XX monoclonal antibody.

XX

OS Homo sapiens.

XX

XX WO200190193-A1.

XX

PD 29-NOV-2001.

XX

XX 24-MAY-2001; 2001WO-US016864.

XX

PR 24-MAY-2000; 2000US-00577930.

XX

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX

PI Abrahamson JA, Kikly KK;

XX

DR WPI: 2002-083094/11.

XX

XX Novel monoclonal antibody that binds to human sialoadhesin factor-3 for

PT treating or preventing cancer, inflammation, autoimmunity, allergy,

PT asthma, rheumatoid arthritis, multiple sclerosis, AIDS and infections.

XX

PS Claim 13; Page 67; 69pp; English.

XX

CC The invention relates to monoclonal antibodies that bind to human

CC sialoadhesin factor-3 (SAF-3). SAF-3 antibody is useful for treating or

CC preventing cancer, inflammation, autoimmunity, allergy, asthma, central

CC nervous system (CNS) inflammation, rheumatoid arthritis, multiple

CC sclerosis, AIDS and bacterial, fungal, protozoan and viral infections and

CC for modulating an immune response in a mammal, where the immune response

CC is downregulated or enhanced. SAF-3 antibody is useful as diagnostic and

CC therapeutic reagents, to subcharacterise cell populations during

CC haematopoietic development, to treat anaemia, as a diagnostic marker to

CC distinguish between different forms of cancer, to purge bone marrow ex

CC vivo of cancer cells expressing SAF-3, as a tool to aid in the ex vivo

CC expansion (proliferation and/or differentiation) of haematopoietic

CC progenitor cells expressing SAF-3, as a stimulus in vivo for stem cell

CC mobilisation into the periphery and as an vivo chemoprotective agent.

CC Protein comprising immunoglobulin complementarity determining region

CC (CDR) of SAF-3 antibody and its nucleic acid is useful to configure

CC screening methods for detecting the effect of added compounds on the

CC production of mRNA and polypeptide in cells. The present sequence is

CC complementarity determining region of human monoclonal antibody (mAb)

CC 12B1 light chain variable region (VK), which binds to SAF-3

XX

SO Sequence 9 AA:

Query Match 33.0%; Score 32; DB 5; Length 9;

Best Local Similarity 83.3%; Pred. No. 2.1e+06;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 8 NIPYPT 13

DB 4 NIPYPT 9

RESULT 12

AEF76312

ID AEF76312 standard; protein; 9 AA.

XX

AC AEF76312;

XX

DT 20-APR-2006 (first entry)

XX

DE Prostate cancer cell antibody light chain CDR3 SEQ ID NO:65.

XX

XX antibody; prostate tumor; cytostatic; andrology; genitourinary disease;

XX neoplasm; antibody identification; antibody therapy; light chain.

XX

OS Mus musculus.

XX

XX WO2006017173-A1.

XX

PD 16-FEB-2006.

XX

XX 08-JUL-2005; 2005WO-US024260.

XX

XX 10-JUL-2004; 2004US-0586811P.

XX

XX (ALEX-) ALEXION PHARM INC.

XX

PI Bowdish KS, Xin H, Vantiri F, Siva A;

XX

DR WPI: 2006-173528/18.

XX

XX New antibody that binds to a prostate cancer cell, useful for detecting

PT cancerous cells in vivo, for killing or ablating prostate cancer cells in

PT vivo, and for delivering a variety of cytotoxic drugs.

XX

PS Claim 16; SEQ ID NO 65; 48pp; English.

XX

XX The invention relates to an antibody (I) that binds to a prostate cancer

CC cell. Also described are the following: identifying (M) antibodies

CC specific to cancer cells; generating a phage displayed antibody library

CC using cells collected from subjects immunized with cancer cells, removing

CC members of the library that bind to human red blood cells to generate a

CC sub-library, and recovering from the sub-library members that display

CC antibodies that bind to the cancer cell, or contacting cancer cells with
CC a hapten, generating a phage displayed antibody library using cells
CC collected from subjects immunized with cancer cells, removing members of
CC the library that bind to human red blood cells to generate a sub-library,
CC and recovering from the sub-library members that display antibodies that
CC bind to the cancer cell; an isolated nucleic acid (II) encoding (I); an
CC expression vector (III) comprising (II); a host cell (IV) transfected
CC with (III); and an antibody that binds to Cdcpl. (VI) is useful for
CC identifying antibodies specific to cancer cells. (I) is useful as a
CC therapeutic for cancer, for detecting cancerous cells in vivo, for
CC killing or ablating cancerous cells in vivo (preferably prostate cancer
CC cells), and for delivering a variety of cytotoxic drugs including
CC therapeutic drugs, a compound emitting radiation, molecules of plants,
CC fungal or bacterial origin, biological proteins, and their mixtures. The
CC present sequence represents prostate cancer cell antibody light chain
CC CDR3 SEQ ID NO:65.
XX
SQ Sequence 9 AA;

Query Match 33.0%; Score 32; DB 10; Length 9;
Best Local Similarity 83.3%; Pred. No. 2.1e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 NIPPT 13
Db 4 NIPPT 9

RESULT 13
ADT40399
ID ADT40399 standard; peptide; 11 AA.
XX
AC ADT40399;
XX
DT 30-DEC-2004 (first entry)
XX
DE hSARS virus peptide, SEQ ID 1387.
XX
KM Virucide; Severe Acute Respiratory Syndrome; SARS; vaccine.
XX
OS SARS coronavirus.
XX
PN WO2004085650-A1.
XX
PD 07-OCT-2004.
XX
PF 24-MAR-2004; 2004WO-CN000246.
XX
PR 24-MAR-2003; 2003US-0457031P.
PR 26-MAR-2003; 2003US-0457730P.
PR 02-APR-2003; 2003US-0459931P.
PR 03-APR-2003; 2003US-0460357P.
PR 08-APR-2003; 2003US-0461265P.
PR 14-APR-2003; 2003US-0462805P.
PR 23-APR-2003; 2003US-0464886P.
PR 25-APR-2003; 2003US-0465738P.
PR 14-MAY-2003; 2003US-0470935P.
XX
PA (UYHK-) UNIV HONG KONG.
XX
PI Chan K, Guan Y, Nicholas JM, Peiris JSM, Poon L, Yuen K;
PI Leung FC;
XX
DR WPI; 2004-737326/72.
XX
PT New nucleic acid molecule encoding nucleocapsid- or spike-gene protein of
PT a human Severe Acute Respiratory Syndrome (hSARS) virus, useful for
PT diagnosing and treating SARS.
XX
PS Example; SEQ ID NO 1387; 200P; English.
XX
CC The present invention relates to novel human Severe Acute Respiratory
CC Syndrome (hSARS) viral nucleic acid and protein sequences derived from a

CC hSARS virus having China Center for Type Culture Collection Deposit
CC Accession No. CCTCC-V200303. The present invention also relates to novel
CC nucleic acid molecules (I; ADT41483 or ADT41485) encoding a nucleocapsid-
CC (N) or spike (S)-gene protein of a hSARS virus. Also disclosed are
CC methods for detecting the presence of a N- or S-gene of the hSARS virus
CC or of the protein in a biological sample and identifying a subject
CC infected with the hSARS virus. The hSARS virus, nucleic acid and protein
CC sequences are useful as vaccines for diagnosing or treating SARS. They
CC are also useful in clinical and scientific research applications. The
CC hSARS virus genome (ADT39027) was obtained and the amino acid sequences
CC of all three reading frames were deduced from the complementary strand.
CC ADT40120 is the full-length protein encoded by the first reading frame of
CC the complementary strand and ADT40121-ADT40601 are the peptides from the
CC first reading frame protein. ADT40602 is the full-length protein encoded
CC by the second reading frame of the complementary strand and ADT40603-
CC ADT40976 are the peptides from the second reading frame protein. ADT40977
CC is the full-length protein encoded by the third reading frame of the
CC complementary strand and ADT40978-ADT41482 are the peptides from the
CC third reading frame protein.
XX
SQ Sequence 11 AA;

Query Match 33.0%; Score 32; DB 8; Length 11;
Best Local Similarity 54.5%; Pred. No. 3e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 GQKATNIPPT 13
Db 1 GQSQSNILPPT 11

RESULT 14
ADT79816
ID ADT79816 standard; protein; 11 AA.
XX
AC ADT79816;
XX
DT 30-DEC-2004 (first entry)
XX
DE SARS virus complementary DNA strand reading frame 1 protein #279.
XX
KM Virucide; vaccine; detection; severe acute respiratory syndrome;
KM real-time quantitative polymerase chain reaction; SARS.
XX
OS SARS coronavirus.
XX
PN WO2004085455-A1.
XX
PD 07-OCT-2004.
XX
PF 24-MAR-2004; 2004WO-CN000247.
XX
PR 24-MAR-2003; 2003US-0457031P.
PR 26-MAR-2003; 2003US-0457730P.
PR 02-APR-2003; 2003US-0459931P.
PR 03-APR-2003; 2003US-0460357P.
PR 08-APR-2003; 2003US-0461265P.
PR 14-APR-2003; 2003US-0462805P.
PR 23-APR-2003; 2003US-0464886P.
PR 05-MAY-2003; 2003US-0468139P.
PR 16-MAY-2003; 2003US-0471200P.
XX
PA (UYHK-) UNIV HONG KONG.
XX
PI Chan K, Guan Y, Nicholas JM, Peiris JSM, Poon L, Yuen K;
PI WPI; 2004-737292/72.
XX
DR WPI; 2004-737292/72.
XX
PT New isolated nucleic acid molecule useful for detecting, treating,
PT ameliorating, or preventing the virus causing severe acute respiratory
PT syndrome in humans using a real-time quantitative polymerase chain
PT reaction assay.
XX

PS Example; SEQ ID NO 1387, 183pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule consisting
CC essentially of, and/or hybridizes under stringent conditions to a fully
CC defined nucleotide sequence of 16-25 base pairs (bp; SEQ ID NO: 2471-
CC 2476), or its complement. The methods and compositions of the present
CC invention are useful for the detection of the virus causing Severe Acute
CC Respiratory Syndrome (SARS) in humans using a real-time quantitative
CC polymerase chain reaction (PCR) assay. They can also be used in treating,
CC ameliorating, managing or preventing SARS. This sequence corresponds to a
CC partial SARS protein sequence from the complementary reading frame 1.
XX
SQ Sequence 11 AA;

Query Match 33.0%; Score 32; DB 8; Length 11;
Best Local Similarity 54.5%; Pred. No. 3e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 3 GOKATNIFPYT 13
Db 1 GOSOSNLPOT 11

RESULT 15
ADT37929
ID ADT37929 standard; peptide; 11 AA.
XX
AC ADT37929;
XX
DT 30-DEC-2004 (first entry)
XX
DE hSARS virus peptide, SEQ ID 1387.
XX
KM Vitucide; Severe Acute Respiratory Syndrome; SARS; vaccine.
XX
KW SARS coronavirus.
XX
OS
XX
PN MO2004085633-A1.
XX
PD 07-OCT-2004.
XX
PF 24-MAR-2004; 2004MO-CN000248.
XX
PR 24-MAR-2003; 2003US-0457031P.
PR 26-MAR-2003; 2003US-0457730P.
PR 02-APR-2003; 2003US-0459931P.
PR 03-APR-2003; 2003US-0460357P.
PR 08-APR-2003; 2003US-0461265P.
PR 14-APR-2003; 2003US-0462805P.
PR 23-APR-2003; 2003US-0464886P.
XX
PA (UYHK-) UNIV HONG KONG.
XX
PI Chan K, Guan Y, Nicholls JM, Peiris JSM, Poon L, Yuen K,
PI Leung PC;
XX
DR WPI; 2004-728736/71.
XX
PT New isolated human severe acute respiratory syndrome (hSARS) virus,
PT useful as vaccine for diagnosing or treating SARS or in clinical and
PT scientific research applications.
XX
PS Example; SEQ ID NO 1387, 176pp; English.
XX
CC The present invention relates to novel human Severe Acute Respiratory
CC Syndrome (hSARS) viral nucleic acid and protein sequences derived from a
CC hSARS virus having China Center for Type Culture Collection Deposit
CC Accession No. CCTCC-V200303. The hSARS virus, nucleic acid and protein
CC sequences are useful as vaccines or vaccines for diagnosing or treating SARS. They
CC are also useful in clinical and scientific research applications. The
CC hSARS virus genome (ADT36557) was obtained and the amino acid sequences
CC of all three reading frames were deduced from the complementary strand of
CC ADT37650 is the full-length protein encoded by the first reading frame of

CC the complementary strand and ADT37651-ADT38131 are the peptides from the
CC first reading frame protein. ADT38132 is the full-length protein encoded
CC by the second reading frame of the complementary strand and ADT38133-
CC ADT38506 are the peptides from the second reading frame protein. ADT38507
CC is the full-length protein encoded by the third reading frame of the
CC complementary strand and ADT38508-ADT39012 are the peptides from the
CC third reading frame protein.
XX
SQ Sequence 11 AA;

Query Match 33.0%; Score 32; DB 8; Length 11;
Best Local Similarity 54.5%; Pred. No. 3e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 3 GOKATNIFPYT 13
Db 1 GOSOSNLPOT 11

Search completed: May 30, 2006, 15:04:08
Job time : 61.6667 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 30, 2006, 15:17:23 ; Search time 49.3333 Seconds
(without alignments)
169.011 Million cell updates/sec

Title: US-10-758-165A-10
Perfect score: 97
Sequence: 1 VDGGKATNIFPYTAPGKQ 18

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues
Total number of hits satisfying chosen parameters: 432914

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /EMC_Celextra_SIDS3/ptocdata/2/pubppaa/US07_PUBCOMB.pep:*
2: /EMC_Celextra_SIDS3/ptocdata/2/pubppaa/US08_PUBCOMB.pep:*
3: /EMC_Celextra_SIDS3/ptocdata/2/pubppaa/US09_PUBCOMB.pep:*
4: /EMC_Celextra_SIDS3/ptocdata/2/pubppaa/US10A_PUBCOMB.pep:*
5: /EMC_Celextra_SIDS3/ptocdata/2/pubppaa/US10B_PUBCOMB.pep:*
6: /EMC_Celextra_SIDS3/ptocdata/2/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	DB ID	Description
1	97	100.0	18	5	US-10-758-165-10
2	87	89.7	18	5	US-10-758-165-9
3	55	56.7	18	5	US-10-758-165-12
4	37	38.1	15	5	US-10-836-118-34
5	35	36.1	18	5	US-10-758-165-11
6	34	35.1	15	4	US-10-052-788-5
7	32	33.0	9	3	US-09-920-262A-6
8	32	33.0	9	5	US-10-912-994-6
9	32	33.0	9	5	US-10-975-883-6
10	32	33.0	9	5	US-10-975-740A-6
11	32	33.0	9	5	US-10-975-708-6
12	32	33.0	9	5	US-10-246-019A-14
13	32	33.0	11	5	US-10-808-187-1387
14	32	33.0	11	6	US-10-807-807-1387
15	32	33.0	11	6	US-11-004-399-2080
16	32	33.0	15	4	US-10-107-532-5915
17	32	33.0	15	4	US-10-107-532-5915
18	32	33.0	15	4	US-10-107-532-5915
19	32	33.0	15	4	US-10-107-532-5915
20	32	33.0	15	4	US-10-530-061-1511
21	32	33.0	15	4	US-10-530-061-1511
22	32	33.0	15	4	US-10-530-061-1511
23	32	33.0	15	4	US-10-530-061-1511
24	32	33.0	15	4	US-10-530-061-1511
25	32	33.0	15	4	US-10-530-061-1511
26	32	33.0	15	4	US-10-530-061-1511
27	32	33.0	15	4	US-10-530-061-1511

28	29	29.9	9	6	US-11-009-040A-214	Sequence 214, App
29	29	29.9	9	6	US-11-009-073A-214	Sequence 214, App
30	29	29.9	9	6	US-11-009-769A-214	Sequence 214, App
31	29	29.9	12	3	US-09-813-653-26	Sequence 26, App
32	29	29.9	15	5	US-10-865-478-786	Sequence 786, App
33	29	29.9	15	5	US-10-720-831-70	Sequence 20, App
34	29	29.9	17	4	US-10-306-631-76	Sequence 76, App
35	29	29.9	18	4	US-10-654-200-28	Sequence 28, App
36	29	29.9	18	4	US-10-654-200-29	Sequence 29, App
37	29	29.9	18	4	US-10-846-548A-1	Sequence 1, App
38	28	28.9	9	4	US-10-160-506-34	Sequence 34, App
39	28	28.9	9	4	US-10-449-379-34	Sequence 34, App
40	28	28.9	9	4	US-10-688-015-34	Sequence 34, App
41	28	28.9	9	4	US-10-160-505-34	Sequence 34, App
42	28	28.9	9	5	US-10-482-284A-186	Sequence 186, App
43	28	28.9	9	6	US-11-218-813-34	Sequence 34, App
44	28	28.9	10	4	US-10-281-652-18	Sequence 18, App
45	28	28.9	10	5	US-10-691-157-18	Sequence 18, App

ALIGNMENTS

RESULT 1
US-10-758-165-10
; Sequence 10, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammettberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Felis catus
US-10-758-165-10

Query Match 100.0%; Score 97; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. NO. 6.2e-09;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGGKATNIFPYTAPGKQ 18
Db 1 VDGGKATNIFPYTAPGKQ 18

RESULT 2
US-10-758-165-9
; Sequence 9, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammettberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US/10758,165
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-758-165-9

Query Match 89.7%; Score 87; DB 5; Length 18;

Best Local Similarity 100.0%; Pred. No. 2.9e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGGKATNIPFYTAPG 16
Db 1 VDGGKATNIPFYTAPG 16

RESULT 3

US-10-758-165-12
; Sequence 12, Application US/10758165
; Publication No. US20050196816a1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758.165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Sus scrofa
US-10-758-165-12

Query Match 56.7%; Score 55; DB 5; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.061;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VDGGKATNIPFYTAP 15
Db 1 VDGGEDRNLFSTYAP 15

RESULT 4

US-10-856-118-34
; Sequence 34, Application US/10856118
; Publication No. US20050025747a1
; GENERAL INFORMATION:
; APPLICANT: Laidlaw, Stephen
; APPLICANT: Skinner, Mike
; APPLICANT: Hill, Adrian V.S.
; APPLICANT: Gilbert, Sarah C.
; APPLICANT: Anderson, Richard
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: 3742.1000-000
; CURRENT APPLICATION NUMBER: US/10/856.118
; CURRENT FILING DATE: 2004-05-27
; PRIOR APPLICATION NUMBER: PCT/GB02/005411
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: GB0128733.3
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/334,649
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Flanking sequence
US-10-856-118-34

Query Match 38.1%; Score 37; DB 5; Length 15;
Best Local Similarity 55.6%; Pred. No. 50;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 7 TNIFPYTAP 15
||::|||

Db 2 TNVYPYDVP 10

RESULT 5

US-10-758-165-11
; Sequence 11, Application US/10758165
; Publication No. US20050196816a1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758.165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Equus caballus
US-10-758-165-11

Query Match 36.1%; Score 35; DB 5; Length 18;
Best Local Similarity 44.4%; Pred. No. 1.3e+02;
Matches 8; Conservative 1; Mismatches 9; Indels 0; Gaps 0;

Qy 1 VDGGKATNIPFYTAPGKQ 18
Db 1 IDGGKVDEQFPQHGVLVKQ 18

RESULT 6

US-10-052-788-5
; Sequence 5, Application US/10052788
; Publication No. US20030087314a1
; GENERAL INFORMATION:
; APPLICANT: Gershwin, Laurel J.
; APPLICANT: Pettigrew, Howard David
; APPLICANT: Kalina, Warren V.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Epsilon Immunoglobulin Chain Derived Peptides for
; FILE REFERENCE: 023070-121000US
; CURRENT APPLICATION NUMBER: US/10/052.788
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: epitope peptide
; OTHER INFORMATION: P5, middle portion of C2 of equine IGF epsilon
; OTHER INFORMATION: heavy chain
US-10-052-788-5

Query Match 35.1%; Score 34; DB 4; Length 15;
Best Local Similarity 54.5%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 VDGGKATNIFP 11
Db 2 IDGGKVDEQFP 12

RESULT 7

US-09-920-262A-6
; Sequence 6, Application US/09920262A
; Publication No. US20030124123a1
; GENERAL INFORMATION:
; APPLICANT: Shealy, David

```

; APPLICANT: Knight, David
; APPLICANT: Scallion, Bernie
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Peritt, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0248
; CURRENT APPLICATION NUMBER: US/09/920,262A
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/223,358
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/236,827
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-920-262A-6
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Query Match          33.0%; Score 32; DB 3; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.9e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      8 NIPYPT 13
      ||:||||
Db       4 NIPYPT 9
```

```

RESULT 8
US-10-912-994-6
; Sequence 6, Application US/10912994
; Publication No. US2005002937A1
; GENERAL INFORMATION:
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Knight, David
; APPLICANT: Peritt, David
; APPLICANT: Scallion, Bernie
; APPLICANT: Shealy, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0248DIV1
; CURRENT APPLICATION NUMBER: US/10/912,994
; CURRENT FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 60/223,358
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 60/236,827
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 09/920,262
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-912-994-6
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```
Query Match          33.0%; Score 32; DB 5; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.9e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      8 NIPYPT 13
      ||:||||
Db       4 NIPYPT 9
```

```

RESULT 9
US-10-975-883-6
; Sequence 6, Application US/10975883
; Publication No. US20050112127A1
; GENERAL INFORMATION:
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Knight, David
```

```

; APPLICANT: Peritt, David
; APPLICANT: Scallion, Bernie
; APPLICANT: Shealy, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES AND USES
; FILE REFERENCE: CEN0248DIV04
; CURRENT APPLICATION NUMBER: US/10/975,883
; CURRENT FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: US 60/223,358
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 60/236,827
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 09/920,262
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-975-883-6
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Query Match          33.0%; Score 32; DB 5; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.9e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      8 NIPYPT 13
      ||:||||
Db       4 NIPYPT 9
```

```

RESULT 10
US-10-975-740A-6
; Sequence 6, Application US/10975740A
; Publication No. US20050196838A1
; GENERAL INFORMATION:
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Knight, David
; APPLICANT: Peritt, David
; APPLICANT: Scallion, Bernie
; APPLICANT: Shealy, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES AND NUCLEIC ACIDS
; FILE REFERENCE: CEN0248DIV03
; CURRENT APPLICATION NUMBER: US/10/975,740A
; CURRENT FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US 60/223,358
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 60/236,827
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 09/920,262
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-975-740A-6
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Query Match          33.0%; Score 32; DB 5; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.9e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
QY      8 NIPYPT 13
      ||:||||
Db       4 NIPYPT 9
```

```

RESULT 11
US-10-975-708-6
; Sequence 6, Application US/10975708
; Publication No. US20050214293A1
; GENERAL INFORMATION:
; APPLICANT: Giles-Komar, Jill
```

```

; APPLICANT: Knight, David
; APPLICANT: Peritt, David
; APPLICANT: Scallon, Bernie
; APPLICANT: Shealy, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES AND COMPOSITIONS
; FILE REFERENCE: CEN0248DIV02
; CURRENT APPLICATION NUMBER: US/10/975,708
; CURRENT FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: US 60/223,358
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 60/236,827
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 09/920,262
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO: 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-975-708-6
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```

Query Match          33.0%; Score 32; DB 5; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.9e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      8 NIPYPT 13
      ||:||||
Db      4 NIPYPT 9
```

```

RESULT 12
US-10-246-019A-14
; Sequence 14, Application US/10246019A
; Publication No. US20060073133A1
; GENERAL INFORMATION:
; APPLICANT: Kikly, Kristine K.
; APPLICANT: Abrahamson, Julie
; TITLE OF INVENTION: Sialoadhesin Factor-3 Antibodies
; FILE REFERENCE: GHS0019-1C1
; CURRENT APPLICATION NUMBER: US/10/246,019A
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: USSN 09/577,930
; PRIOR FILING DATE: 2000-01-22
; PRIOR APPLICATION NUMBER: USSN 09/046,736
; PRIOR FILING DATE: 1998-03-24
; PRIOR APPLICATION NUMBER: USSN 60/041,885
; PRIOR FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 14
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human
US-10-246-019A-14
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Query Match          33.0%; Score 32; DB 5; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.9e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
QY      8 NIPYPT 13
      ||:||||
Db      4 NIPYPT 9
```

```

RESULT 13
US-10-808-187-1387
; Sequence 1387, Application US/10808187
; Publication No. US2005009009A1
; GENERAL INFORMATION:
; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
```

```

; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN
; TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE
; FILE REFERENCE: V9661.0078
; CURRENT APPLICATION NUMBER: US/10/808,187
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,031
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: 60/457,730
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/459,931
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/460,357
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/461,265
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/462,805
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/468,139
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: 60/464,886
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 60/471,200
; PRIOR FILING DATE: 2003-05-16
; NUMBER OF SEQ ID NOS: 2476
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO: 1387
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human severe acute respiratory system virus
US-10-808-187-1387
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Query Match          33.0%; Score 32; DB 5; Length 11;
Best Local Similarity 54.5%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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```
QY      3 GOKATNIPYPT 13
      ||:||||
Db      1 GOSOSNIPOT 11
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RESULT 14
US-10-807-807-1387
; Sequence 1387, Application US/10807807
; Publication No. US20050181357A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, FREDERICK C.
; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN M.
; TITLE OF INVENTION: A HIGH-THROUGHPUT DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS
; FILE REFERENCE: V9661.0077
; CURRENT APPLICATION NUMBER: US/10/807,807
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,031
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: 60/457,730
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/459,931
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/460,357
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/461,265
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/462,805
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/464,886
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; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 60/465,738
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: 60/470,935
; PRIOR FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 2487
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 1387
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human severe acute respiratory system virus
US-10-807-807-1387

```

```

Query Match      33.0%; Score 32; DB 5; Length 11;
Best Local Similarity 54.5%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

```

```

QY      3 GOKATNIFPYT 13
      ||:|||||
Db      1 GQSQSNILPQT 11

```

```

RESULT 15
US-11-004-399-2080
; Sequence 2080, Application US/11004399
; Publication No. US20060053516A1
; GENERAL INFORMATION:
; APPLICANT: Chye, Mee Lee
; APPLICANT: Li, Hong Ye
; APPLICANT: Ramalingam, Sachikumar
; APPLICANT: Poon, Leo Lit Man
; APPLICANT: Peiris, Joseph Sriyal Malik
; TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-Cov Viral Nucleotide
; FILE REFERENCE: 2587/73166/RDX
; CURRENT APPLICATION NUMBER: US/11/004,399
; PRIOR FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: US 60/527,637
; PRIOR FILING DATE: 2003-12-03
; NUMBER OF SEQ ID NOS: 4043
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2080
; LENGTH: 11
; TYPE: PRT
; ORGANISM: SARS-Cov Virus
US-11-004-399-2080

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Query Match      33.0%; Score 32; DB 6; Length 11;
Best Local Similarity 54.5%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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QY      3 GOKATNIFPYT 13
      ||:|||||
Db      1 GQSQSNILPQT 11

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Search completed: May 30, 2006, 15:20:14
 Job time : 49.3333 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceeleration Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2006, 15:17:53 ; Search time 4 Seconds
(without alignments)
50.118 Million cell updates/sec

Title: US-10-758-165A-10
Sequence: 1 VDGQKATNFPYTPGKQ 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 11137335 residues

Total number of hits satisfying chosen parameters: 11661

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:*
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2: /EMC_Celettera_SIDS3/ptodaca/1/pubppaa/US06_NEW_PUB pep:*
3: /EMC_Celettera_SIDS3/ptodaca/1/pubppaa/US07_NEW_PUB pep:*
4: /EMC_Celettera_SIDS3/ptodaca/1/pubppaa/US08_NEW_PUB pep:*
5: /EMC_Celettera_SIDS3/ptodaca/1/pubppaa/PC7_NEW_PUB pep:*
6: /EMC_Celettera_SIDS3/ptodaca/1/pubppaa/US10_NEW_PUB pep:*
7: /EMC_Celettera_SIDS3/ptodaca/1/pubppaa/US11_NEW_PUB pep:*
8: /EMC_Celettera_SIDS3/ptodaca/1/pubppaa/US60_NEW_PUB pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28.9	9	7	US-11-219-563-34	Sequence 34, Appl
2	26.8	9	7	US-11-254-182-12	Sequence 12, Appl
3	25.8	12	7	US-11-177-358C-16	Sequence 16, Appl
4	25.8	12	7	US-11-177-359C-16	Sequence 16, Appl
5	25.8	12	7	US-11-177-340C-16	Sequence 16, Appl
6	24.7	10	6	US-10-538-066-747	Sequence 747, Appl
7	24.7	16	1	US-09-731-899-19	Sequence 19, Appl
8	23.7	9	6	US-10-522-356-3	Sequence 3, Appl1
9	23.7	9	7	US-11-252-276-38	Sequence 38, Appl
10	23.7	9	7	US-11-023-959A-83	Sequence 83, Appl
11	23.7	10	7	US-11-140-487A-1314	Sequence 1314, Ap
12	23.7	12	7	US-11-106-014-82	Sequence 82, Appl
13	23.7	13	7	US-11-134-228A-8	Sequence 8, Appl1
14	23.7	17	7	US-11-251-734-50	Sequence 30, Appl
15	22.5	12	7	US-11-122-986-799	Sequence 799, Appl
16	22.7	9	7	US-11-297-317-21	Sequence 21, Appl
17	22.7	9	7	US-11-140-487A-211	Sequence 211, App
18	22.7	9	7	US-11-140-487A-348	Sequence 348, Appl
19	22.7	10	7	US-11-140-487A-1346	Sequence 1346, Ap
20	22.7	13	7	US-11-219-121-39	Sequence 39, Appl
21	22.7	14	7	US-11-219-563-10	Sequence 8, Appl1
22	22.7	14	7	US-11-300-563-8	Sequence 812, App
23	22.7	16	7	US-11-122-986-812	Sequence 59, Appl
24	22.7	17	7	US-11-257-498-59	Sequence 52, Appl
25	22.7	17	7	US-11-121-282-52	

26	22	22.7	18	7	US-11-257-498-53	Sequence 53, Appl
27	21	21.6	9	7	US-11-055-093-222	Sequence 120, App
28	21	21.6	9	7	US-11-140-487A-120	Sequence 120, App
29	21	21.6	9	7	US-11-140-487A-551	Sequence 551, App
30	21	21.6	9	7	US-11-140-487A-1446	Sequence 1446, App
31	21	21.6	10	7	US-11-055-093-223	Sequence 223, App
32	21	21.6	10	7	US-11-140-487A-1447	Sequence 1447, Ap
33	21	21.6	10	7	US-11-140-487A-1596	Sequence 1596, Ap
34	21	21.6	11	6	US-10-540-431-11	Sequence 11, Appl
35	21	21.6	11	7	US-11-177-358C-3	Sequence 3, Appl1
36	21	21.6	11	7	US-11-177-359C-3	Sequence 3, Appl1
37	21	21.6	11	7	US-11-177-340C-3	Sequence 3, Appl1
38	21	21.6	11	7	US-11-122-986-800	Sequence 800, Appl
39	21	21.6	12	1	US-09-784-950-21	Sequence 21, Appl
40	21	21.6	12	7	US-11-172-986-656	Sequence 656, App
41	21	21.6	13	7	US-11-211-175-1	Sequence 1, Appl1
42	20	20.6	9	7	US-11-140-487A-8	Sequence 8, Appl1
43	20	20.6	9	7	US-11-140-487A-24	Sequence 24, Appl
44	20	20.6	9	7	US-11-140-487A-212	Sequence 212, App
45	20	20.6	9	7	US-11-140-487A-327	Sequence 327, App

ALIGNMENTS

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RESULT 1
US-11-219-563-34
; Sequence 34, Application US/11219563
; Publication No. US20060088539A1
; GENERAL INFORMATION:
; APPLICANT: Bandier, Neil
; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
; FILE REFERENCE: 13651.001 (BZL-001)
; CURRENT APPLICATION NUMBER: US/11/219, 563
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: PCT/US04/06586
; PRIOR FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: US 10/379, 838
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 10/449, 379
; PRIOR FILING DATE: 2003-05-10
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: PASTESEQ for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-219-563-34
Query Match 28.9%; Score 28; DB 7; Length 9;
Best Local Similarity 63.6%; Pred. No. 5.2e+04;
Matches 7; Conservative 0; Mismatches 2; Indels 2; Gaps 1;
OY 3 GQKATNFPYT 13
DB 1 GQSYT--FPYT 9
RESULT 2
US-11-254-182-12
; Sequence 12, Application US/11254182
; Publication No. US20060088523A1
; GENERAL INFORMATION:
; APPLICANT: ANDYA, JAMES
; APPLICANT: GMEB, SHIANG C.
; APPLICANT: LIU, JUN
; APPLICANT: SHEN, YE
; TITLE OF INVENTION: ANTIBODY FORMULATIONS
; FILE REFERENCE: P2104R1
; CURRENT APPLICATION NUMBER: US/11/254, 182
; CURRENT FILING DATE: 2005-10-19
; PRIOR APPLICATION NUMBER: US 60/620, 413
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PRIOR FILING DATE: 2004-10-20
; NUMBER OF SEQ ID NOS: 74
; SEQ ID NO 12
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-254-182-12

Query Match 26.8%; Score 26; DB 7; Length 9;
Best Local Similarity 80.0%; Pred. No. 5.2e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 IFPYT 13
|:|:|
Db 5 IVPYT 9

RESULT 3
US-11-177-358C-16
; Sequence 16, Application US/1177358C
; Publication No. US20060094072A1
; GENERAL INFORMATION:
; APPLICANT: CAMPBELL, DOUGLAS A.
; TITLE OF INVENTION: PEPTIDE SEQUENCE TAGS AND METHOD OF USING SAME
; FILE REFERENCE: 113703-1006
; CURRENT APPLICATION NUMBER: US/11/177,358C
; CURRENT FILING DATE: 2005-07-11
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
US-11-177-358C-16

Query Match 25.8%; Score 25; DB 7; Length 12;
Best Local Similarity 50.0%; Pred. No. 94;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 FPYTA PGK 17
|:|:|
Db 1 FPDCGPGK 8

RESULT 4
US-11-177-359C-16
; Sequence 16, Application US/1177359C
; Publication No. US20060094058A1
; GENERAL INFORMATION:
; APPLICANT: CAMPBELL, DOUGLAS A.
; TITLE OF INVENTION: PEPTIDE SEQUENCE TAGS AND METHOD OF USING SAME
; FILE REFERENCE: 113703-1004
; CURRENT APPLICATION NUMBER: US/11/177,359C
; CURRENT FILING DATE: 2005-07-11
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
US-11-177-359C-16

Query Match 25.8%; Score 25; DB 7; Length 12;
Best Local Similarity 50.0%; Pred. No. 94;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 FPYTA PGK 17

Db 1 FPDCGPGK 8
|:|:|

RESULT 5
US-11-177-340C-16
; Sequence 16, Application US/1177340C
; Publication No. US20060099663A1
; GENERAL INFORMATION:
; APPLICANT: CAMPBELL, DOUGLAS A.
; TITLE OF INVENTION: PEPTIDE SEQUENCE TAGS AND METHOD OF USING SAME
; FILE REFERENCE: 113703-1005
; CURRENT APPLICATION NUMBER: US/11/177,340C
; CURRENT FILING DATE: 2005-07-11
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
US-11-177-340C-16

Query Match 25.8%; Score 25; DB 7; Length 12;
Best Local Similarity 50.0%; Pred. No. 94;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 FPYTA PGK 17
|:|:|
Db 1 FPDCGPGK 8

RESULT 6
US-10-538-066-747
; Sequence 747, Application US/10538066
; Publication No. US20060094649A1
; GENERAL INFORMATION:
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen
; FILE REFERENCE: 2060.015PC06
; CURRENT APPLICATION NUMBER: US/10/538,066
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US 60/432,017
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 767
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 747
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: A3 non-natural consensus peptide
US-10-538-066-747

Query Match 24.7%; Score 24; DB 6; Length 10;
Best Local Similarity 44.4%; Pred. No. 1.1e+02;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 9 IFPYTAPGK 17
|:|:|
Db 2 VFPPYALINK 10

RESULT 7
US-09-731-899-19
; Sequence 19, Application US/09731899
; Publication No. US20060088548A1
; GENERAL INFORMATION:
; APPLICANT: Chain, Benjamin
; TITLE OF INVENTION: CHIMERIC PEPTIDES AS IMMUNOGENS, ANTIBODIES THERETO, AND METHODS
; FOR IMMUNIZATION USING CHIMERIC PEPTIDES OR ANTIBODIES

Wed May 31 06:05:16 2006

us-10-758-165a-10.closed.rapbn

FILE REFERENCE: 20555/1203433-US1
CURRENT APPLICATION NUMBER: US/09/731,899
CURRENT FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/169,687
PRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.3
SEQ ID NO 19
LENGTH: 16
ORGANISM: Tetanus toxin bacteria
US-09-731-899-19

Query Match 24.7%; Score 24; DB 1; Length 16;
Best Local Similarity 44.4%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 7 TNYFYTAP 15
DB 3 STYVYIGP 11

RESULT 8
US-10-522-356-3

Sequence 3, Application US/10522356
Publication No. US20060105323A1
GENERAL INFORMATION:
APPLICANT: WHITEHAM, CHRISTOPHER BRUCE ALEXANDER
APPLICANT: CLARK, ANTHONY JOHN
TITLE OF INVENTION: MULTI-REPORTER GENE MODEL FOR TOXICOLOGICAL SCREENING
FILE REFERENCE: 102286.155 US1
CURRENT APPLICATION NUMBER: US/10/522.356
CURRENT FILING DATE: 2005-01-26
PRIOR APPLICATION NUMBER: PCT/GB03/003192
PRIOR FILING DATE: 2003-07-25
PRIOR APPLICATION NUMBER: GB 0217402.7
PRIOR FILING DATE: 2002-07-26
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn version 3.3
SEQ ID NO 3
LENGTH: 9
TYPE: PRT
ORGANISM: Unknown
FEATURE: Description of Unknown Sequence: Haemagglutinin
OTHER INFORMATION: epitope from unknown organism
US-10-522-356-3

Query Match 23.7%; Score 23; DB 6; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.2e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 10 FPYTAP 15
DB 1 VPDVDP 6

RESULT 9
US-11-252-276-38

Sequence 38, Application US/11252276
Publication No. US20060094868A1
GENERAL INFORMATION:
APPLICANT: Giuliano, Kenneth A.
APPLICANT: Bright, Gary
APPLICANT: Olsson, Keith
APPLICANT: Burroughs-Tencza, Sarah
TITLE OF INVENTION: A System for Cell Based Screening
FILE REFERENCE: 97-022-K2-CO
CURRENT APPLICATION NUMBER: US/11/252.276
CURRENT FILING DATE: 2005-10-17
PRIOR APPLICATION NUMBER: 09/713,572
PRIOR FILING DATE: 2000-11-15

PRIOR APPLICATION NUMBER: 09/430,656
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: 09/398,965
PRIOR FILING DATE: 1999-09-17
PRIOR APPLICATION NUMBER: 09/031,271
PRIOR FILING DATE: 1998-02-27
PRIOR APPLICATION NUMBER: 08/810,983
PRIOR FILING DATE: 1997-02-27
PRIOR APPLICATION NUMBER: 60/136,078
PRIOR FILING DATE: 1999-05-26
PRIOR APPLICATION NUMBER: 60/106,308
PRIOR FILING DATE: 1998-10-30
NUMBER OF SEQ ID NOS: 168
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 38
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: Description of Artificial Sequence: HA epitope
US-11-252-276-38

Query Match 23.7%; Score 23; DB 7; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.2e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 10 FPYTAP 15
DB 1 VPDVDP 6

RESULT 10
US-11-023-959A-83
Sequence 83, Application US/11023959A
Publication No. US20060106203A1
GENERAL INFORMATION:
APPLICANT: Winter, Greg
TITLE OF INVENTION: Ligand
FILE REFERENCE: 8039/2142
CURRENT APPLICATION NUMBER: US/11/023,959A
CURRENT FILING DATE: 2004-12-28
PRIOR APPLICATION NUMBER: PCT/GB03/002804
PRIOR FILING DATE: 2003-06-30
NUMBER OF SEQ ID NOS: 187
SOFTWARE: PatentIn version 3.3
SEQ ID NO 83
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE: HA tag
OTHER INFORMATION: HA tag
US-11-023-959A-83

Query Match 23.7%; Score 23; DB 7; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.2e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 10 FPYTAP 15
DB 1 VPDVDP 6

RESULT 11
US-11-140-487A-1314
Sequence 1314, Application US/11140487A
Publication No. US20060093617A1
GENERAL INFORMATION:
APPLICANT: Innogenetics N.V.
TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C v.
FILE REFERENCE: 166
CURRENT APPLICATION NUMBER: US/11/140,487A
CURRENT FILING DATE: 2005-05-31
PRIOR APPLICATION NUMBER: EP 04012951.2

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; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: EP 04447239.7
; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: EP 05102441.2
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/576,310
; PRIOR FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: US 60/622,782
; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US 60/665,395
; PRIOR FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2278
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1314
; LENGTH: 10
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-11-140-487A-1314
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Query Match
Best Local Similarity 23.7%; Score 23; DB 7; Length 10;
Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
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QY 9 IFPTAPGKQ 18
DB 1 IYRFVTGER 10
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RESULT 12
US-11-106-014-82
; Sequence 82, Application US/11106014
; Publication No. US2006008846A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, Michele
; APPLICANT: Chiar, Dan Sharim
; APPLICANT: Laties, Esther
; APPLICANT: Seivasca, Promod
; APPLICANT: Chandawarkar, Rajiv
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT
; FILE REFERENCE: 5914-106-999
; CURRENT APPLICATION NUMBER: US/11/106,014
; PRIOR FILING DATE: 2005-04-13
; PRIOR APPLICATION NUMBER: 10/632,150
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 09/385,219
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1997-03-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-106-014-82
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Query Match
Best Local Similarity 23.7%; Score 23; DB 7; Length 12;
Matches 6; Conservative 2; Mismatches 3; Indels 2; Gaps 1;
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QY 2 DGKATIFPYTA 14
DB 2 DGEKDT--YSYLA 12
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RESULT 13
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US-11-134-228A-8
; Sequence 8, Application US/11134228A
; Publication No. US20060105320A1
; GENERAL INFORMATION:
; APPLICANT: Lindquist et al
; TITLE OF INVENTION: ELECTRICAL CONDUCTORS AND DEVICES FROM PRION-LIKE PROTEINS
; FILE REFERENCE: 30554/40155A
; CURRENT APPLICATION NUMBER: US/11/134,228A
; PRIOR FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 60/573,277
; PRIOR FILING DATE: 2004-05-20
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Hemagglutinin
US-11-134-228A-8
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Query Match
Best Local Similarity 23.7%; Score 23; DB 7; Length 13;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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QY 10 FPYAP 15
DB 1 YPYDVP 6
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RESULT 14
US-11-251-734-30
; Sequence 30, Application US/11251734
; Publication No. US20060100134A1
; GENERAL INFORMATION:
; APPLICANT: AVANTIS PHARMACEUTICALS INC.
; APPLICANT: GUO, Yong
; APPLICANT: MORSE, Clarence C
; APPLICANT: YAO, Zhengbin
; TITLE OF INVENTION: MEMBRANE PENETRATING PEPTIDES AND USES THEREOF
; FILE REFERENCE: HMR2053 US NPI
; CURRENT APPLICATION NUMBER: US/11/251,734
; PRIOR FILING DATE: 2005-10-17
; PRIOR APPLICATION NUMBER: US 09/933,780
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/227,647
; PRIOR FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: GB 0103110.3
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-11-251-734-30
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Query Match
Best Local Similarity 23.7%; Score 23; DB 7; Length 17;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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QY 5 KATNIF 10
DB 2 KKTNLF 7
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RESULT 15
US-11-122-986-799
; Sequence 799, Application US/1122986
; Publication No. US20060104989A1
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; GENERAL INFORMATION:
; APPLICANT: EDWARDS, ALED
; APPLICANT: DHARAMSI, AKIL
; APPLICANT: VEDADI, MASOUD
; TITLE OF INVENTION: ESSENTIAL NOVEL BACTERIAL POLYPEPTIDES
; FILE REFERENCE: IPT-330.01
; CURRENT APPLICATION NUMBER: US/11/122,986
; CURRENT FILING DATE: 2005-05-05
; PRIOR APPLICATION NUMBER: 60/423,875
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,832
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,915
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,757
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,758
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/424,367
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,376
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,370
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,362
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,373
; PRIOR FILING DATE: 2002-11-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 844
; SOFTWARE: Patentin Ver. 3.3
; SEQ ID NO 799
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-11-122-986-799

Query Match      23.2%; Score 22.5; DB 7; Length 12;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY      7 TNIFPYTAPG 16
      :|||
Db      1 SNI-PYTMVG 9
```

Search completed: May 30, 2006, 15:20:31
Job time : 4 secs

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-674-973A-64

Query Match
Best Local Similarity 33.0%; Score 32; DB 2; Length 15;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VDQKATNIFP 11
Db 4 VEDQKTLVFP 14

RESULT 3
US-09-865-548A-126
; Sequence 126, Application US/09865548A
; Patent No. 6867283
; GENERAL INFORMATION:
; APPLICANT: Barnea, Eilon
; APPLICANT: Beer, Ilan
; APPLICANT: Ziv, Tamar
; APPLICANT: Admon, Arie
; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECULE
; FILE REFERENCE: 01/22080
; CURRENT APPLICATION NUMBER: US/09/865,548A
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/290,958
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 126
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-865-548A-126

Query Match
Best Local Similarity 30.9%; Score 30; DB 2; Length 9;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 NIFPY 12
Db 1 NIFPY 5

RESULT 4
US-08-333-565-22
; Sequence 22, Application US/08333565
; Patent No. 5622852
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/333,565
; FILING DATE: 31-OCT-1994
; CLASSIFICATION: 435
```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000700
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-333-565-22

Query Match
Best Local Similarity 30.9%; Score 30; DB 1; Length 17;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 PYTARG 16
Db 3 PYLARG 8

RESULT 5
US-08-661-479-22
; Sequence 22, Application US/08661479
; Patent No. 5834209
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/661,479
; FILING DATE: 11-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/333,565
; FILING DATE: 31-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000700
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-661-479-22

Query Match
Best Local Similarity 83.3%; Score 30; DB 1; Length 17;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 11 PYTARG 16
Db 3 PYLARG 8
RESULT 6
US-09-042-353-366
Sequence 366, Application US/09042353
Patent No. 6255458
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 421
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/042,353
FILING DATE: 13-MAR-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-OCT-1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/758,417
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 01-DEC-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 014643-009040US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 366:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-042-353-366
Query Match 29.9%; Score 29; DB 2; Length 9;
Best Local Similarity 83.3%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 8 NIPYPT 13
Db 4 NSFPT 9
RESULT 7
US-08-758-417A-214
Sequence 214, Application US/08758417A
Patent No. 6300129
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 417
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,417A
FILING DATE: 02-DEC-1996
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/165,699
FILING DATE: 10-DEC-1993
APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 08/096,762

;; FILING DATE: 22-JUL-1993
;; APPLICATION NUMBER: US 08/053,131
;; FILING DATE: 26-APR-1993
;; APPLICATION NUMBER: US 07/990,860
;; FILING DATE: 16-DEC-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Serafini, Andrew T.
;; REGISTRATION NUMBER: 41,303
;; REFERENCE/DOCKET NUMBER: 014643-009030US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0300
;; TELEFAX: (415) 576-0200
;; INFORMATION FOR SEQ ID NO: 214:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 9 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: <Unknown>
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; SEQUENCE DESCRIPTION: SEQ ID NO: 214:
US-08-758-417A-214

Query Match 29.9%; Score 29; DB 2; Length 9;
Best Local Similarity 83.3%; Pred. No. 5e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 NIFPYT 13
Db 4 NSFPT 9

RESULT 8
US-09-307-265A-14
; Sequence 14, Application US/09307265A
; Patent No. 6225456
; GENERAL INFORMATION:
; APPLICANT: Gu, Trent
; APPLICANT: Orlica, Satoshi
; APPLICANT: Han, Min
; TITLE OF INVENTION: RAS SUPPRESSOR SUR-5
; FILE REFERENCE: UTC-03732
; CURRENT APPLICATION NUMBER: US/09/307,265A
; CURRENT FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 14
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-307-265A-14

Query Match 29.9%; Score 29; DB 2; Length 11;
Best Local Similarity 62.5%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 11 PYTAGTK 18
Db 1 PYTSGKK 8

RESULT 9
US-08-278-774-20
; Sequence 20, Application US/08278774
; Patent No. 6653450
; GENERAL INFORMATION:
; APPLICANT: Berg, Richard A
; APPLICANT: Toman, David P
; APPLICANT: Wallace, Donald
; TITLE OF INVENTION: MUTATED RECOMBINANT COLLAGENS
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COLLAGEN CORPORATION
; STREET: 2500 Faber Place

;; CITY: Palo Alto
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94303
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/278,774
;; FILING DATE: 22-JUL-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Rafayko, Kathi L
;; REGISTRATION NUMBER: 36,644
;; REFERENCE/DOCKET NUMBER: 94-018
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 354-4642
;; TELEFAX: (415) 354-4752
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 20:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 15 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-278-774-20

Query Match 29.9%; Score 29; DB 2; Length 15;
Best Local Similarity 41.7%; Pred. No. 3.6e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 VDQKATNIPY 12
Db 2 IGGERKAGGFAPY 13

RESULT 10
US-09-526-195-9
; Sequence 9, Application US/09526195
; Patent No. 6699478
; GENERAL INFORMATION:
; APPLICANT: Hancock, Gerald E.
; APPLICANT: Tebbey, Paul W.
; TITLE OF INVENTION: ENHANCED IMMUNE RESPONSE TO ATTACHMENT
; FILE REFERENCE: 1646.1030-004
; CURRENT APPLICATION NUMBER: US/09/526,195
; CURRENT FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: US 60/084,863
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: PCT/US98/19656
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: US 60/059,684
; PRIOR FILING DATE: 1997-09-19
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-09-526-195-9

Query Match 29.9%; Score 29; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 3.6e+02;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 7 TNIPPYTAGTK 18

Db 1 TTILASTPGVK 12

RESULT 11

US-08-957-130-19
; Sequence 19, Application US/08957130
; Patent No. 6280959
; GENERAL INFORMATION:
; APPLICANT: WO, Xue-Ru
; APPLICANT: SUN, Tung-Tien
; TITLE OF INVENTION: METHOD FOR SCREENING COMPOUNDS FOR
; TITLE OF INVENTION: INHIBITING BACTERIAL ATTACHMENT TO HOST CELL RECEPTORS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 Seventh Street N.W., Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/957,130
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: SUN=8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-957-130-19

Query Match 29.9%; Score 29; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 3.8e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 4; Gaps 1;

Qy 5 KATNIFPYTAPGK 18
Db 4 QVTNL----APGK 13

RESULT 12

US-09-856-920-1
; Sequence 1, Application US/09856920
; Patent No. 6740325
; GENERAL INFORMATION:
; APPLICANT: Veda Research and Development Co.
; TITLE OF INVENTION: Peptide-based vaccine for influenza
; FILE REFERENCE: 9822 PCT
; CURRENT APPLICATION NUMBER: US/09/856,920
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Influenza virus
US-09-856-920-1

Query Match 29.9%; Score 29; DB 2; Length 18;

Best Local Similarity 44.4%; Pred. No. 4.3e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 7 TNIPPYTAP 15
Db 5 SNCYPPYDVP 13

RESULT 13

US-09-641-803-18
; Sequence 18, Application US/09641803
; Patent No. 6500798
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDGOH, Istvan
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND
; TITLE OF INVENTION: ANALOGS THEREOF AS OXIDATIVE STRESS REGULATORS
; FILE REFERENCE: 265,00220101
; CURRENT APPLICATION NUMBER: US/09/641,803
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,310
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-641-803-18

Query Match 28.9%; Score 28; DB 2; Length 10;
Best Local Similarity 42.9%; Pred. No. 3.3e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 9 IPYPTAP 15
Db 1 VYPTGP 7

RESULT 14

US-09-641-802-18
; Sequence 18, Application US/09641802
; Patent No. 6852685
; GENERAL INFORMATION:
; APPLICANT: BOLDGOH, Istvan
; TITLE OF INVENTION: TO PROMOTE NEURAL CELL DIFFERENTIATION
; FILE REFERENCE: 265,00240101
; CURRENT APPLICATION NUMBER: US/09/641,802
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,633
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-641-802-18

Query Match 28.9%; Score 28; DB 2; Length 10;
Best Local Similarity 42.9%; Pred. No. 3.3e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 9 IPYPTAP 15
Db 1 VYPTGP 7

Db 1 VYPFTGP 7

RESULT 15
US-09-641-801-18
; Sequence 18, Application US/09641801
; Patent No. 6903068
; GENERAL INFORMATION:
; APPLICANT: STANTON, G. John
; APPLICANT: HUGHES, Thomas K.
; APPLICANT: BOLDOGH, Istvan
; APPLICANT: GEORGIADES, Jerzy
; TITLE OF INVENTION: USE OF COLOSTRININ, CONSTITUENT PEPTIDES THEREOF, AND ANALOG
; TITLE OF INVENTION: THEREOF
; TITLE OF INVENTION: FOR INDUCING CYTOKINES
; FILE REFERENCE: 265.00230101
; CURRENT APPLICATION NUMBER: US/09/641,801
; CURRENT FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: 60/149,311
; PRIOR FILING DATE: 1999-08-17
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-09-641-801-18

Query Match 28.9%; Score 28; DB 2; Length 10;
Best Local Similarity 42.9%; Pred. No. 3.3e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 9 IFPYTAP 15
::|||
Db 1 VYPFTGP 7

Search completed: May 30, 2006, 15:09:25
Job time : 20.3333 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 30, 2006, 15:04:28 ; Search time 12 Seconds
(without alignments)
144.325 Million cell updates/sec

Title: US-10-758-165A-9

Perfect score: 97
Sequence: 1 VDGKATNIFPYTAPGK 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3215

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28.9	15	2	I53284	T-cell receptor be
2	27.8	15	2	PA0099	phenotypic variati
3	27.8	17	2	H49048	T-cell receptor be
4	27.8	18	2	A59137	protein P11 - gold
5	26.8	18	2	A61577	24k serine protein
6	25.8	15	2	D28587	T-cell receptor be
7	25.8	15	2	R28587	T-cell receptor be
8	25.8	16	2	B28587	T-cell receptor be
9	25.8	16	2	F53284	T-cell receptor be
10	24.7	14	2	B58502	36k kidney stone p
11	24.7	15	2	PH1318	ig heavy chain DJ
12	24.7	17	2	S18534	hypothetical prote
13	24.7	18	2	A25941	ig heavy chain J-H
14	23.7	12	2	C20907	ig kappa-1 chain J
15	23.7	13	2	S23640	ig kappa chain J s
16	23.7	13	2	CS3275	ig kappa-1 chain J
17	23.7	15	2	B45115	peptidylprolyl iso
18	23.7	16	2	S03532	ig heavy chain J r
19	23.7	16	2	PS0383	ig heavy chain J r
20	23.7	16	2	S38292	30k allergen - rye
21	23.7	18	2	PQ0072	T-cell receptor be
22	23.7	18	2	S20322	gluten - wheat
23	23.7	18	2	CS6046	urinary tract ston
24	22.7	12	2	PQ0786	NMDH2 dehydrogenas
25	22.7	13	2	S01904	H+-transporting tw
26	22.7	14	2	PH1306	ig heavy chain DJ
27	22.7	15	2	PA0056	protein QP200002 -
28	22.7	15	2	PA0087	cytochrome c2 - fu
29	22.7	17	2	C84063	hypothetical prote

30	21	21.6	10	2	S71948	matrix metalloprot
31	21	21.6	10	2	A39745	endo-glucosylceram
32	21	21.6	12	2	A53524	ubiquinol-cytochro
33	21	21.6	14	2	PL0142	carbon-monoxide de
34	21	21.6	14	2	S59495	formate dehydrogen
35	21	21.6	15	2	B61457	alpha-glucosidase
36	21	21.6	15	2	S36893	ribosomal protein
37	21	21.6	16	2	E53284	T-cell receptor be
38	21	21.6	17	2	S50901	chlorophyll a/b-bi
39	21	21.6	18	2	S57518	T cell receptor be
40	21	21.6	18	2	S70612	alpha-macroglobuli
41	20	20.6	9	2	D48186	ATPase RI subunit
42	20	20.6	9	2	S10784	enamelin i - bovin
43	20	20.6	13	2	B58533	CD61 homolog - cha
44	20	20.6	14	2	S22236	lipoxigenase (EC 1
45	20	20.6	14	2	G44957	photosystem II oxy

ALIGNMENTS

RESULT 1
I53284
T-cell receptor beta 2 chain J region, Jbeta2.7 - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 02-May-1994 #sequence #revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: I53284
R:Harindranath, N.; Alexander, C.B.; Mage, R.G.
Mol. Immunol. 28, 881-888, 1991
A:Title: Evolutionarily conserved organization and sequences of germline diversity and
A:Reference number: A53284; MUID:91342695; PMID:1678859
A:Accession: I53284
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-15 <HAR>
A:Cross-references: UNIPARC:UPI0000115418; GB:S60737; NID:9233916; PIDN:AA019525.1; PID
A>Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIPI:60747)
C:Keywords: T-cell receptor

Query Match 28.9%; Score 28; DB 2; Length 15;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 YTAGTK 18
DB 5 YFGPGTK 11

RESULT 2
PA0099
Phenotypic variation protein - fungus (Fusarium sporotrichioides) (fragment)
C:Species: Fusarium sporotrichioides
C:Date: 20-Feb-1995 #sequence #revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: PA0099
R:Chow, L.P.; Fukaya, N.; Sugiyura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPD, October 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotric
A:Reference number: PA0099
A:Accession: PA0099
A:Molecule type: protein
A:Residues: 1-15 <CHO>
A:Cross-references: UNIPROT:Q7M4Y7; UNIPARC:UPI0000178405

Query Match 27.8%; Score 27; DB 2; Length 15;
Best Local Similarity 62.5%; Pred. No. 3.2e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 FPYTAGCT 17
DB 7 FKYSASGT 14

RESULT 3

H49048
T-cell receptor beta chain V region (CDR3 junction, clone Vbeta20.1) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
C/Accession: H49048
R:Stoud, M.; Kjelsgaard-Kragh, J.; Suleyman, S.; Vinje, O.; Natvig, J.B.; Forre, O.
Eur. J. Immunol. 22, 2413-2416, 1992
A/Title: Limited heterogeneity of T cell receptor variable region gene usage in juvenile
A/Reference number: A49048; MUID:92387250; PMID:11387614
A/Accession: H49048
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-17 <STO>
A/Cross-references: UNIPARC:UPI0000176DF0
A/Experimental source: patient SS, IL-2R+ synovial T-cells
A/Note: sequence extracted from NCBI backbone (NCBIF:113270)
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: T-cell receptor

Query Match 27.8%; Score 27; DB 2; Length 17;
Best Local Similarity 62.5%; Pred. No. 3.6e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 6 ATNIFPYT 13
| | | | |
DB 8 AWTFFPYT 15

RESULT 4
A59137
protein P11 - golden needle mushroom (fragment)
C/Species: Flammulina velutipes (golden needle mushroom)
C/Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004
C/Accession: A59137
R:Sakamoto, Y.; Ando, A.; Tamai, Y.; Miura, K.
A/Title: Differences of proteins expressed in the fruiting dikaryon and the non-fr
submitted to the Protein Sequence Database, November 1999
A/Description: Differences of proteins expressed in the fruiting dikaryon and the non-fr
A/Reference number: A59137
A/Accession: A59137
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-18 <SAK>
A/Cross-references: UNIPROT:Q7M4W6; UNIPARC:UPI000017CB27

Query Match 27.8%; Score 27; DB 2; Length 18;
Best Local Similarity 80.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 11 PYTAP 15
| | | | |
DB 2 PYTSP 6

RESULT 5
A61577
24k serine proteinase (PC 3.4.21.-) - Streptomyces fradiae (fragment)
C/Species: Streptomyces fradiae
C/Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C/Accession: A61577
R:Singh, U.; Wolz, S.A.; Lad, P.J.
Int. J. Biochem. 23, 979-984, 1991
A/Title: Two new extracellular serine proteases from Streptomyces fradiae.
A/Reference number: A61577; MUID:92155439; PMID:1766859
A/Accession: A61577
A/Molecule type: protein
A/Residues: 1-18 <SIN>
A/Cross-references: UNIPROT:Q7M198; UNIPARC:UPI000017AB13
C/Keywords: extracellular protein; hydrolase; serine proteinase

Query Match 26.8%; Score 26; DB 2; Length 18;
Best Local Similarity 41.7%; Pred. No. 5.7e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 VDGOKATNIFPY 12
| | | | |
DB 2 VGGTRAAQGFPPW 13

RESULT 6
D28587
T-cell receptor beta-2 chain J-B2.5 segment - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 05-Nov-1999
C/Accession: D28587
R:Toyonaga, B.; Yoshikai, Y.; Vadasz, V.; Chin, B.; Mak, T.W.
Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985
A/Title: Organization and sequences of the diversity, joining, and constant region gene
A/Reference number: A94081; MUID:86094276; PMID:3866244
A/Accession: D28587
A/Molecule type: DNA
A/Residues: 1-15 <TOY>
A/Cross-references: UNIPARC:UPI0000113C7C; GB:M14159; NID:g338852; PIDN:AAA60679.1; PID
C/Keywords: T-cell receptor

Query Match 25.8%; Score 25; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 6.9e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 12 YTAGGTK 18
| | | | |
DB 5 YFGPGTR 11

RESULT 7
F28587
T-cell receptor beta-2 chain J-B2.7 segment - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 05-Nov-1999
C/Accession: F28587
R:Toyonaga, B.; Yoshikai, Y.; Vadasz, V.; Chin, B.; Mak, T.W.
Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985
A/Title: Organization and sequences of the diversity, joining, and constant region gene
A/Reference number: A94081; MUID:86094276; PMID:3866244
A/Accession: F28587
A/Molecule type: DNA
A/Residues: 1-15 <TOY>
A/Cross-references: UNIPARC:UPI0000113C7E; GB:M14159; NID:g338852; PIDN:AAA60681.1; PID
C/Keywords: T-cell receptor

Query Match 25.8%; Score 25; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 6.9e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 12 YTAGGTK 18
| | | | |
DB 5 YFGPGTR 11

RESULT 8
B28587
T-cell receptor beta-2 chain J-B2.3 segment - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 05-Nov-1999
C/Accession: B28587
R:Toyonaga, B.; Yoshikai, Y.; Vadasz, V.; Chin, B.; Mak, T.W.
Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985
A/Title: Organization and sequences of the diversity, joining, and constant region gene
A/Reference number: A94081; MUID:86094276; PMID:3866244
A/Accession: B28587
A/Molecule type: DNA
A/Residues: 1-16 <TOY>
A/Cross-references: UNIPARC:UPI000002FDD6; GB:M14159; NID:g338852; PIDN:AAA60677.1; PID
C/Keywords: T-cell receptor

Query Match 25.8%; Score 25; DB 2; Length 16;
Best Local Similarity 57.1%; Pred. No. 7.4e+02;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 12 YTAAGTK 18
| | | |
| | | |

Db 6 YFGPGTR 12

RESULT 9

F53284

T-cell receptor beta 2 chain J region, Jbeta2.3 - rabbit

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999

C/Accession: F53284

R:Harindranath, N.; Alexander, C.B.; Mage, R.G.

Mol. Immunol. 28, 881-888, 1991

A/Title: Evolutionarily conserved organization and sequences of germline diversity and J

A/Reference number: A53284; MUID:91342695; PMID:1678859

A/Accession: F53284

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-16 <HNR>

A/Cross-references: UNIPARC:UPI0000115415; GB:S60737; NID:g233916; PIDN:AA19522.1; PID:

A/Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIPI:60744)

C/Keywords: T-cell receptor

Query Match 25.8%; Score 25; DB 2; Length 16;

Best Local Similarity 57.1%; Pred. No. 7.4e+02;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 12 YTAAGTK 18
| | | |
| | | |

Db 6 YFGPGTR 12

RESULT 10

B58502

36k kidney stone protein - unidentified bacterium (fragment)

C/Species: unidentified bacterium

C/Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 10-Jul-1998

C/Accession: B58502

R:Binette, J.P.; Binette, M.B.

submitted to the Protein Sequence Database, October 1996

A/Description: The proteins of kidney and gallbladder stones.

A/Reference number: A58501

A/Accession: B58502

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-14 <BIN>

A/Cross-references: UNIPARC:UPI000017A8D0

A/Note: tentative identification of 8-Tyr and 9-Trp

Query Match 24.7%; Score 24; DB 2; Length 14;

Best Local Similarity 66.7%; Pred. No. 9.5e+02;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 NIFPYT 13
| | | |
| | | |

Db 4 NIFGPT 9

RESULT 11

PH1318

Ig heavy chain DJ region (clone C527-121) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C/Accession: PH1318

R:Wasserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

J. Exp. Med. 176, 1577-1581, 1992

A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph

A/Reference number: PH1302; MUID:93094761; PMID:1460419

A/Accession: PH1318

A/Molecule type: DNA

A/Residues: 1-15 <MAS>

A/Cross-references: UNIPARC:UPI000017C244

C/Keywords: heterotetramer; immunoglobulin

Query Match 24.7%; Score 24; DB 2; Length 15;

Best Local Similarity 45.5%; Pred. No. 1e+03;

Matches 5; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 7 TNIFPYTAPGT 17
| | | | |
| | | | |

Db 5 TGTFDVGQGT 15

RESULT 12

S18534

hypothetical protein 7 (eryG 3' region) - Saccharopolyspora erythraea (fragment)

C/Species: Saccharopolyspora erythraea

C/Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 07-Apr-1994

C/Accession: S18534

R:Haydock, S.F.; Dowson, J.A.; Dillon, N.; Roberts, G.A.; Cortes, J.; Leadlay, P.F.

Mol. Gen. Genet. 230, 120-128, 1991

A/Title: Cloning and sequence analysis of genes involved in erythromycin biosynthesis I

methylintransferases.

A/Reference number: S18530; MUID:92079866; PMID:1840640

A/Accession: S18534

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-17 <HMY>

A/Cross-references: UNIPARC:UPI000017AD81; EMBL:X60379

A/Note: the authors translated the codon CTG for residue 12 as Gly

Query Match 24.7%; Score 24; DB 2; Length 17;

Best Local Similarity 62.5%; Pred. No. 1.2e+03;

Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 IFPYTAG 16
| | | | |
| | | | |

Db 1 IFPAVASG 8

RESULT 13

A25941

Ig heavy chain J-H1 region - rat (fragment)

C/Species: Rattus norvegicus (Norway rat)

C/Date: 03-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 23-Jul-1999

C/Accession: A25941; JH0666

R:Bruggemann, M.; Free, J.; Diamond, A.; Howard, J.; Cobbold, S.; Waldmann, H.

Proc. Natl. Acad. Sci. U.S.A. 83, 6075-6079, 1986

A/Title: Immunoglobulin heavy chain locus of the rat: striking homology to mouse antibo

A/Reference number: A25941; MUID:86287397; PMID:3016742

A/Accession: A25941

A/Molecule type: DNA

A/Residues: 1-18 <BRU>

A/Cross-references: UNIPARC:UPI0000114C27; DB:M13798; NID:g204707; PIDN:AAA1371.1; PID

R:Lang, P.; Mochkat, R.

Gene 102, 261-264, 1991

A/Title: Immunoglobulin heavy-chain joining genes in the rat: comparison with mouse and

A/Reference number: JH0666; MUID:91340162; PMID:1908401

A/Accession: JH0666

A/Molecule type: DNA

A/Residues: 1-18 <LAN>

A/Cross-references: UNIPARC:UPI0000114C27; EMBL:X56791

C/Superfamily: Immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

Query Match 24.7%; Score 24; DB 2; Length 18;

Best Local Similarity 50.0%; Pred. No. 1.3e+03;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 PPTAPGT 17
| | | | |
| | | | |

Db 5 PFWGPGT 12

RESULT 14

C20907
 IG kappa-1 chain J3 region - rabbit
 C/Species: Oryctolagus cuniculus (domestic rabbit)
 C/Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 16-Aug-1996
 C/Accession: C20907
 R:Emorine, L.; Max, E.E.
 Nucleic Acids Res. 11, 8877-8890, 1983
 A/Title: Structural analysis of a rabbit immunoglobulin kappa2 J-C locus reveals multiple
 A/Reference number: A20907; MUID:84169523; PMID:6324107
 A/Accession: C20907
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-12 <EMO>
 A/Cross-references: UNIPARC:UPI000017C5CP
 C/Keywords: heterotetramer; immunoglobulin

Query Match

Best Local Similarity 23.7%; Score 23; DB 2; Length 12;
 Pred. No. 1.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PGTK 18

DB 5 PGTK 8

RESULT 15

S23640
 IG kappa chain J segment (J-kappa-3) - human
 C/Species: Homo sapiens (man)
 C/Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
 C/Accession: S23640
 R:Huber, C.; Klobeck, H.G.; Zachau, H.G.
 Eur. J. Immunol. 22, 1561-1565, 1992
 A/Title: Ongoing V(kappa)-J(kappa) recombination after formation of a productive V(kappa)
 A/Reference number: S23637; MUID:92289816; PMID:1601042
 A/Accession: S23640
 A/Status: preliminary; nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-13 <HUB>
 A/Cross-references: UNIPARC:UPI0000116784; EMBL:X63370
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1991
 C/Keywords: heterotetramer; immunoglobulin

Query Match

Best Local Similarity 23.7%; Score 23; DB 2; Length 13;
 Pred. No. 1.3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PGTK 18

DB 5 PGTK 8

Search completed: May 30, 2006, 15:08:21
 Job time : 13 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 30, 2006, 15:01:11 ; Search time 68.6667 Seconds
(without alignments)
242.480 Million cell updates/sec

Title: US-10-758-165A-9

Perfect score: 97
Sequence: 1 VDCQKXATNTPYTPAPGTX 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 12648

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 7.2:*
1: uniprot_sprot:*
2: uniprot_tramb1:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	35.1	17	2	046473_FELCA
2	32	33.0	8	2	070Y88_9LAMI
3	28.5	29.4	18	2	09TWL4_IUCCU
4	28	28.9	16	2	03ZEV4_9CHAR
5	27.5	28.4	16	2	08LIY7_PLEBO
6	27	27.8	15	2	07M4Y7_FUSSP
7	27	27.8	16	2	03ZEV6_9CHAR
8	27	27.8	18	2	07M4W6_FLAWE
9	27	27.8	18	2	03TW38_MOUSE
10	26	26.8	15	1	CWP16_LYCES
11	26	26.8	15	2	07S007_NEUCR
12	26	26.8	18	2	07M198_STRFR
13	25	25.8	15	2	09URE3_EMENT
14	24	24.7	14	2	07I4T5_SCRYP
15	24	24.7	15	2	069142_STRPY
16	24	24.7	16	2	03ZEV7_9CHAR
17	24	24.7	17	2	065Y26_HORSE
18	23	23.7	8	2	05ZEV7_HUMAN
19	23	23.7	10	2	09ZIB1_CLOPI
20	23	23.7	14	1	CWP27_TOBAC
21	23	23.7	14	1	F78359_HUMAN
22	23	23.7	15	2	05DAR7_9CYAN
23	23	23.7	15	2	085HM7_MOTFL
24	23	23.7	16	2	07M263_SECCF
25	23	23.7	16	2	08LIY8_9CYAN
26	23	23.7	16	2	089560_HHVB
27	23	23.7	16	2	03ZEB7_9CHAR
28	23	23.7	16	2	03ZEW2_9CHAR
29	23	23.7	16	2	03ZEW8_9CHAR
30	23	23.7	16	2	03ZEX1_9CHAR
31	23	23.7	16	2	03ZEX3_9CHAR

32	23	23.7	16	2	03ZEV9_9CHAR	03ZEV9 tringa eryt
33	23	23.7	16	2	03ZEV5_9CHAR	03ZEV5 catopropho
34	23	23.7	16	2	05R3U1_XENLA	05R3U1 xenopus lae
35	23	23.7	17	2	09PRU8_CHICK	09PRU8 gallus gall
36	23	23.7	18	2	07M4Q7_HUMAN	07M4Q7 homo sapien
37	23	23.7	18	2	07MIG0_WHEAT	07MIG0 triticum ae
38	22	22.7	8	2	059AE6_HUMAN	059AE6 homo sapien
39	22	22.7	10	2	07IVN2_MOUSE	07IVN2 mus musculu
40	22	22.7	11	1	PVK1_PERYR	P4657 periphaeti
41	22	22.7	12	2	07M2G3_VICFA	07M2G3 vicia faba
42	22	22.7	14	2	07OY94_9LAMI	07OY94 ocimum grat
43	22	22.7	15	2	07M4Z7_FUSSP	07M4Z7 fusarium sp
44	22	22.7	15	2	09TRE5_BOVIN	09TRE5 bos taurus
45	22	22.7	15	2	09TRN8_PIG	09TRN8 sus scrofa

ALIGNMENTS

```

RESULT 1
046473_FELCA PRELIMINARY; PRT; 17 AA.
ID 046473_FELCA
AC 046473;
DT 01-JUN-1998, integrated into UniProtKB/TrEMBL.
DT 01-JUN-1998, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE Lactase dehydrogenase A (Fragment).
GN Name=LDHA;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC Felinae; Felis.
OC NCBI_TaxID=9685;
OX [1]
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=domesticus;
RC MEDLINE=97141918; PubMed=8988168;
RX Lyons L.A., Laughlin T.F., Copeland N.G., Jenkins N.A., Womack J.E.,
RA O'Brien S.J.;
RT "Comparative anchor tagged sequences (CATS) for integrative mapping of
mammalian genomes.";
RL Nat. Genet. 15:47-56(1997).
CC
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CC
DR EMBL; AF012095; AAC00072.2; -; Genomic_DNA.
FT NON_TER
FT 1
FT 17
FT NON_TER
SQ SEQUENCE 17 AA; 2018 MW; E47943B2E187C1FC CRC64;
Query Match 35.1%; Score 34; DB 2; Length 17;
Best local similarity 46.2%; Pred. No. 2.9e+02;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Db 3 GORVNIFFPTAP 15
3 GORVNIFFPTAP 15
RESULT 2
070Y88_9LAMI PRELIMINARY; PRT; 8 AA.
ID 070Y88_9LAMI
AC 070Y88;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Ribosomal protein (Fragment).
GN Name=Ips16;
OS Platosoma fimbriatum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

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OC asteride; lamids; lamiales; Lamnaceae; Nepetoideae; Ocimeae;
OC Platanostoma.
OX NCBI_TaxID=204168;
RN [1]
RP NUCLEOTIDE SEQUENCE. DOI=10.1016/j.ympev.2003.08.002;
RX PubMed=15019625; PubMed=15019625; Stude S., Otieno D., Grayer R., Harley M.M.,
RA Paton A., Springate D.A., Stude S., Otieno D., Grayer R., Harley M.M.,
RA Willis F., Simonds M.S.J., Powell M.P., Savolainen V.,
RT "Phylogeny and evolution of basil and allies (Ocimeae, Labiatae)
RL based on three plastid DNA regions."
RL Mol. Phylogenet. Evol. 31:277-299(2004).
CC -----
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CC -----
DR EMBL: A505368; CAD5489.1; -; Genomic_DNA.
DR GO: GO:0003735; F:structural constituent of ribosome; IEA.
KM Ribosomal protein.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 789 MW; 86786772D1B84772 CRC64;

Query Match 33.0%; Score 32; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 2.8e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 PYTAPG 16
DB 2 PYTAPG 7

RESULT 3
Q9TWL4_LUCCU PRELIMINARY; PRT; 18 AA.
ID Q9TWL4_LUCCU PRELIMINARY; PRT; 18 AA.
AC Q9TWL4;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE 25 kDa chymotrypsin-like enzyme (Fragment).
OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Megaloptera; Diptera; Brachycera; Muscomorpha; Oestroidea;
OC Calliphoridae; Lucilia.
OX NCBI_TaxID=7375;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=95219141; PubMed=7704304;
RA Casu R.E., Pearson R.D., Jarney J.M., Cadogan L.C., Riding G.A.,
RA Tellam R.L.;
RT "Excretory/secretory chymotrypsin from Lucilia cuprina: purification,
RT enzymatic specificity and amino acid sequence deduced from mRNA.";
RL Insect Mol. Biol. 3:201-211(1994).
CC -----
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CC -----
SQ SEQUENCE 18 AA; 1922 MW; 352EB0729B126B11 CRC64;

Query Match 29.4%; Score 28.5; DB 2; Length 18;
Best Local Similarity 58.3%; Pred. No. 2.5e+03;
Matches 7; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 2 DGOKAT-NIPY 12
DB 3 NGOKATVQGFY 14

RESULT 4
Q3ZEV4_9CHAR PRELIMINARY; PRT; 16 AA.
ID Q3ZEV4_9CHAR PRELIMINARY; PRT; 16 AA.
AC Q3ZEV4;
DT 27-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 27-SEP-2005, sequence version 1.

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DT 07-FEB-2006, entry version 3.
DE ATP synthase F0 subunit 8 (Fragment).
GN Name=ATP8;
OS Tringa totanus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Aves; Neognathae; Charadriiformes; Scolopacidae; Tringa.
OX NCBI_TaxID=171271;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Pereira S.L., Baker A.J.;
RT "Multiple gene evidence for parallel evolution and retention of
RT ancestral morphological states in the shanks (Charadriiformes;
RT Scolopacidae)";
RL Condor 107:514-526(2005).
CC -----
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CC -----
DR EMBL: AY894271; AA94014.1; -; Genomic_DNA.
DR GO: GO:0005739; C:mitochondrion; IEA.
KM Mitochondrion.
FT NON_TER 1 1
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1965 MW; 75D680373ACF82D CRC64;

Query Match 28.9%; Score 28; DB 2; Length 16;
Best Local Similarity 54.5%; Pred. No. 2.7e+03;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 7 TNIPYTPAGT 17
DB 6 TKITPTWTPWT 16

RESULT 5
Q8LIY7_PLEBO PRELIMINARY; PRT; 16 AA.
ID Q8LIY7_PLEBO PRELIMINARY; PRT; 16 AA.
AC Q8LIY7;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Proteolysis-inducing tag (Fragment).
OC Bacteria; Cyanobacteria; Oscillatoriales; Lepidogynya.
OX NCBI_TaxID=1184;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=UTEX 485;
RX MEDLINE=21970088; PubMed=11972342; DOI=10.1093/nar/30.9.2025;
RA Williams K.P.;
RT "Descent of a split RNA.";
RL Nucleic Acids Res. 30:2025-2030(2002).
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CC -----
DR EMBL: AY082652; AA003311.1; -; Genomic_DNA.
FT NON_TER 1 1
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1640 MW; 60FE5985B9B00982 CRC64;

Query Match 28.4%; Score 27.5; DB 2; Length 16;
Best Local Similarity 53.8%; Pred. No. 3.3e+03;
Matches 7; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 6 ATNIFPY---TAP 15
DB 1 ANNIVPAPKATAP 13

RESULT 6
Q7M4Y7_FUSSP PRELIMINARY; PRT; 15 AA.
ID Q7M4Y7_FUSSP PRELIMINARY; PRT; 15 AA.
AC Q7M4Y7;

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DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Phenotypic variation protein (Fragment).
OS Fusarium sporotrichioides.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
OX NCBI_TaxID=5514;
RN [1]
RP PROTEIN SEQUENCE.
RA Chow L.P., Fukaya N., Sugiyura Y., Ueno Y., Tabuchi K., Tsugita A.;
RL Submitted (OCT-1994) to the PIR data bank.
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DR PIR, PA0099, PA0099.
FT NON_TER 1 15
SQ SEQUENCE 15 AA; 1648 MW; 4C4FAFA966995807 CRC64;

Query Match 27.8%; Score 27; DB 2; Length 15;
Best Local Similarity 62.5%; Pred. No. 3.7e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 PPYPATGT 17
DB 7 FRTSASGT 14

RESULT 7
Q3ZEY6_9CHAR PRELIMINARY; PRT; 16 AA.
ID Q3ZEY6_9CHAR
AC Q3ZEY6_9CHAR
DT 27-SEP-2005, integrated into UniProtKB/TrEMBL.
DT 27-SEP-2005, sequence version 1.
DT 07-FEB-2006, entry version 3.
DE ATP synthase F0 subunit 8 (Fragment).
GN Name=ATP8;
OS Tringa flavipes.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauromorpha; Aves; Neognathae; Charadriiformes; Scolopacidae; Tringa.
OX NCBI_TaxID=161739;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Pereira S.L., Baker A.J.;
RT "Multiple gene evidence for parallel evolution and retention of
RT ancestral morphological states in the shanks (Charadriiformes:
RT Scolopacidae).";
RL Condor 107:514-526(2005).

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DR EMBL: AY894261; AAX93984.1; -; Genomic_DNA.
DR GO: GO:0005739; C:mitochondrion; IEA.
KM Mitochondrion.
FT NON_TER 1 1
SQ SEQUENCE 16 AA; 1893 MW; 6FF802724F1F82D CRC64;

Query Match 27.8%; Score 27; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 4e+03;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 6 ATNIPYPATGT 17
DB 5 ATKTTPTWTPWT 16

RESULT 8
Q7M4W6_FLAVE PRELIMINARY; PRT; 18 AA.
ID Q7M4W6_FLAVE

AC Q7M4W6;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Protein P11 (Fragment).
OS Flammulina velutipes.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Agaricales; Tricholomataceae; Flammulina.
OX NCBI_TaxID=38945;
RN [1]
RP PROTEIN SEQUENCE.
RA Sakamoto Y., Ando A., Tamai Y., Miura K.;
RL Submitted (NOV-1999) to the PIR data bank.
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DR PIR, A59137, A59137.
FT NON_TER 1 18
SQ SEQUENCE 18 AA; 1956 MW; FB0434B0AF005AEC CRC64;

Query Match 27.8%; Score 27; DB 2; Length 18;
Best Local Similarity 80.0%; Pred. No. 4.5e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 PYTAP 15
DB 2 PYTSP 6

RESULT 9
Q3TW38_MOUSE
ID Q3TW38_MOUSE PRELIMINARY; PRT; 18 AA.
AC Q3TW38;
DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Osteoclast-like cell cDNA, RIKEN full-length enriched library,
DE clone:1420034D23 product:RNA binding motif, single stranded
DE interacting protein 1, full insert sequence. (Fragment).
GN Name=Rbms1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Methods Enzymol. 303:19-44(1999).

RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Bremner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.U., Wilming L.G., Aldins V., Allen J.E.,
RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla B., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Hummelbeck L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,

RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matzuda H., Matsuwaga S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottegu-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Oriando V., Reed K.C., Pavan W.J., Pavese G., Pesole G.,
RA Petrovsky N., Piazza S., Pang K.C., Reid J.F., Ring B.Z., Ringwald M.,
RA Post B., Ruan Y., Salzberg S.L., Sanderlin A., Seno S., Seese L., Sheng Y.,
RA Schonbach C., Sekiguchi K., Sempé C.A., Seno S., Sinclair B., Taki K.,
RA Shibata K., Shimada H., Shimada K., Silva D., Takenaka Y., Taki K.,
RA Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Tegner J.,
RA Tamajo K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide M., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlestedt C., Matlick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Karayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Imanura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Niimiyu N.,
RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.,
RA "the transcriptional landscape of the mammalian genome";
RA Science 309:1559-1563(2005).
[3]
RA NUCLEOTIDE SEQUENCE.
RA STRAIN=C57BL/6J;
RA PubMed=16141073; DOI=10.1126/science.1112009;
RA RIKEN Genome Exploration Research Group, and Genome Science Group
RA (Genome Network Core Team) and the FANTOM Consortium;
RA "Antisense Transcription in the Mammalian Transcriptome";
RA Science 309:1564-1566(2005).
[4]
RA NUCLEOTIDE SEQUENCE.
RA STRAIN=C57BL/6J;
RA MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Nikaido I., Oseato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schirm L.M., Kanapin A., Matsuda H., Batalov S., Belsel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Fraser K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawagawa Y., Kedzierzki R.W., King B.L.,
RA Konegaya A., Kurochkin I.V., Lee Y., Lemhard B., Lyons P.A.,
RA Meglert D.R., Maltale L., Marchionni L., McKenzie L., Miki H.,
RA Nagaishi T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sanderlin A., Schneider C., Sempé C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
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RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
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RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.,
RA "Analysis of the mouse transcriptome based on functional annotation of
RA 60,770 full-length cDNAs";
RA Nature 420:563-573(2002).
[5]
RA NUCLEOTIDE SEQUENCE.
RA STRAIN=C57BL/6J;
RA MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadoya K., Matzuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann T., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirm L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carinini P., de Bonaldo M.F.,
RA Brakenstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli U., Mombarts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schonbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
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RA "Functional annotation of a full-length mouse cDNA collection";
RA Nature 409:685-690(2001).
[6]
RA NUCLEOTIDE SEQUENCE.
RA STRAIN=C57BL/6J;
RA MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carinini P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
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RA prepare full-length cDNA libraries for rapid discovery of new genes";
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RA NUCLEOTIDE SEQUENCE.
RA STRAIN=C57BL/6J;
RA MEDLINE=20530913; PubMed=11076661; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carinini P.,
RA Konno H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashtwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RA "RIKEN integrated sequence analysis (RISA) system-84-Format
RA sequencing pipeline with 384 multicapillary sequencer";
RA Genome Res. 10:1757-1771(2000).
[8]
RA NUCLEOTIDE SEQUENCE.
RA STRAIN=C57BL/6J;
RA Arakawa T., Carinini P., Fukuda S., Hashizume W., Hayashida K.,
RA Kawai J., Iida J., Imanura K., Imotani K., Itoh M., Kanagawa S.,
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Wataniki A.,
RA Muramatsu M., Hayashizaki Y.,
RA Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL: AK159851; BAB35428.1; -- mRNA.
CC MGI: MGI:1861774; Rpmst1.
DR GO: GO:0005634; C:nucleus; RCA.
DR GO: GO:0003690; F:double-stranded DNA binding; RCA.
DR GO: GO:0003722; F:RNA binding; RCA.
DR GO: GO:0003697; F:single-stranded DNA binding; RCA.
DR GO: GO:0006260; P:DNA replication; RCA.
FT NON TER 1 1
SQ SEQUENCE 18 AA; 2003 MW; 82F8AB5FD94EEA14 CRC64;
Query Match 27.8%; Score 27; DB 2; Length 18;
Best Local Similarity 62.5%; Pred. No. 4.5e-03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 10

CMP16 LYCES
ID CMP16 LYCES STANDARD; PRT; 15 AA.
AC P80812;
DT 25-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DT 25-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE 40 kDa cell wall protein (Fragment).
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Asterids; Lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
OX NCBI_TaxID=4081;
[1]
RP PROTEIN SEQUENCE, AND SUBCELLULAR LOCATION.
RX MEDLINE=97332671; PubMed=9188482; DOI=10.1074/jbc.272.25.15841;
RA Robertson D., Mitchell G.P., Gilroy J.S., Gerrish C., Bolwell G.P.,
RA Slabas A.R.;
RT "Differential extraction and protein sequencing reveals major
RT differences in patterns of primary cell wall proteins from plants.";
RL J. Biol. Chem. 272:15841-15848(1997).
CC -!- SUBCELLULAR LOCATION: Cell wall.
CC
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CC
CC -----
CC Cell wall; Direct protein sequencing.
FT CHAIN 1 >15 /FTid=PRO_0000079677.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1705 MW; 1F328E5C82CA77BE CRC64;

Query Match 26.8%; Score 26; DB 1; Length 15;
Best Local Similarity 44.4%; Pred. No. 5.5e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 10 PFYTPAGTK 18
Db 6 PFYTVQANR 14

RESULT 11
ID Q7S007 NEUCR PRELIMINARY; PRT; 15 AA.
AC Q7S007;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Predicted protein.
GN ORFNames=NCU09752.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
[1]
RP NITROBETIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=74-OR23-1A / FGSC 9871;
RX MEDLINE=22598136; PubMed=12712197; DOI=10.1038/nature01554;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Bell-Pedersen D., Nelson M.A.,
RA Werner-Washburne M., Selitrenikoff C.P., Kinsey J.A., Braun E.L.,
RA Zelter A., Schulte U., Kothe G.O., Jedd G., Mewes H.-W., Staben C.,
RA Marcotte E., Greenberg D., Roy A., Foley K., Naylor J.,
RA Gauger-Tromann N., Barrett R., Gnerre S., Kamal M., Kamyssealis M.,
RA Mauceli E., Bielek C., Rudd S., Fishman D., Krystofova S.,
RA Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S., Cogoni C.,
RA Macioni G., Catchpole D.E.A., Li W., Pratt R.J., Omani S.A.,
RA Desouza C.P.C., Glas N.L., Ozbach M.J., Berglund J.A., Voelker R.,
RA Yarden O., Plamann W., Seiler S., Dunlap J.C., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebdole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nuebaum C., Birren B.W.;
RT "The genome sequence of the filamentous fungus Neurospora crassa.";

RL Nature 422:859-868(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC
CC -----
CC EMBL; AABX01000580; EAA28619.1; -; Genomic DNA.
DR SEQUENCE 15 AA; 1832 MW; 012D0180ABCT089D CRC64;

Query Match 26.8%; Score 26; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 5.5e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 8 NIPPYT 13
Db 2 NVFEYT 7

RESULT 12
ID Q7M198 STRFR PRELIMINARY; PRT; 18 AA.
AC Q7M198;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE 24k serine proteinase (EC 3.4.21.-) (Fragment).
OS Streptomyces fradiae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1906;
[1]
RP PROTEIN SEQUENCE.
RX MEDLINE=92155439; PubMed=1786859; DOI=10.1016/0020-711X(91)90133-8;
RA Sinha U., Wolt S.A., Lad P.J.;
RT "Two new extracellular serine proteases from Streptomyces fradiae.";
RL Int. J. Biochem. 23:979-984(1991).
CC
CC Copyrighted by the UniProt Consortium, see <http://www.uniprot.org/terms>
CC Distributed under the Creative Commons Attribution-NonDerivs License
CC
CC -----
CC PIR: A61577; A61577. 1
DR PIR: A61577; A61577. 1
FT NON_TER 18 18
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2004 MW; 6D6DA167845934A5 CRC64;

Query Match 26.8%; Score 26; DB 2; Length 18;
Best Local Similarity 41.7%; Pred. No. 6.7e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 VDGGKATNIPY 12
Db 2 VGGTRAAQEPFW 13

RESULT 13
ID Q9UR63 EMENI PRELIMINARY; PRT; 15 AA.
AC Q9UR63;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Beta-D-FRUCTOFURANOSIDE FRUCTOHYDROLASE 60 kDa high molecular weight
DE isoform (EC 3.2.1.26) (Fragment).
OS Emericella nidulans (Aspergillus nidulans).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; Emericella.
OX NCBI_TaxID=162425;
[1]
RP PROTEIN SEQUENCE.
RX MEDLINE=96409246; PubMed=8814228; DOI=10.1016/0167-4838(96)00073-8;
RA Chen J.S., Saxton J., Hemming F.W., Peberdy J.F.;

```

RT      "Purification and partial characterization of the high and low
RT      molecular weight form (S- and F-form) of invertase secreted by
RT      Aspergillus nidulans."
RL      Biochim. Biophys. Acta 1296:207-218(1996).
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NonDerivs License
CC      -----
DR      GO:0004564; F:beta-fructofuranosidase activity; IEA.
SQ      SEQUENCE 15 AA; 1588 MW; 2C992B42211366BB CRC64;

Query Match      25.8%; Score 25; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 8.1e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      11 PYTAP 15
      |||
      10 PYTER 14

RESULT 14
Q714T5_9CRYP PRELIMINARY; PRT; 14 AA.
AC  Q714T5;
DT  05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT  05-JUL-2004, sequence version 1.
DT  07-FEB-2006, entry version 7.
DE  tmRNA proteolysis tag (fragment).
GN  Name=sstA;
OS  Rhodomonas salina.
OC  Plastid.
OC  Eukaryota; Cryptophyta; Cryptomonadaceae; Rhodomonas.
OX  NCBI_TaxID=52970;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=CCMP1319;
RX  PubMed=14681369; DOI=10.1093/nar/gkh102;
RA  Guenau de Nova P., Williams K.P.;
RT  "The tmRNA website: reductive evolution of tmRNA in plastids and other
RT  endosymbionts."
RL  Nucleic Acids Res. 32:D104-D108(2004).
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NonDerivs License
CC      -----
DR      EMBL; AF550355; AAQ12671.1; -; Genomic_DNA.
FT  NON TER 1
SQ      SEQUENCE 14 AA; 1528 MW; D995F9B3698210B9 CRC64;

Query March      24.7%; Score 24; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.1e+04;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      6 ATNIFYPT 13
      |||
      1 ANNIVPS 8

RESULT 15
O69142_STRPY PRELIMINARY; PRT; 15 AA.
AC  O69142;
DT  01-AUG-1998, integrated into UniProtKB/TrEMBL.
DT  01-AUG-1998, sequence version 1.
DT  07-FEB-2006, entry version 14.
DE  Protein SIC (fragment).
GN  Name=sic;
OS  Streptococcus pyogenes.
OC  Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC  Streptococcus.
OX  NCBI_TaxID=1314;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.

```

```

RC  STRAIN=AP1;
RX  MEDLINE=98298075; PubMed=9632622;
RA  Berge A., Rasmussen M., Bjork L.;
RT  "Identification of an insertion sequence located in a region encoding
RT  virulence factors of Streptococcus pyogenes."
RL  Infect. Immun. 66:3449-3453(1998).
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NonDerivs License
CC      -----
DR      EMBL; AF064540; AAC38769.1; -; Genomic_DNA.
FT  NON TER 1
SQ      SEQUENCE 15 AA; 1552 MW; 87655FEF847401FF CRC64;

Query Match      24.7%; Score 24; DB 2; Length 15;
Best Local Similarity 40.0%; Pred. No. 1.2e+04;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      8 NIPYTPAGT 17
      ::|||
      6 SVTPYTPSAT 15

```

Search completed: May 30, 2006, 15:07:40
 Job time : 70.6667 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 30, 2006, 14:59:31 ; Search time 61.6667 Seconds
(without alignments)
133.458 Million cell updates/sec

Title: US-10-758-165a-9

Percent score: 97

Sequence: 1 VDGQKATNIPFYTAPEGK 18

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 902922

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8.*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*
10: Geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	97	100.0	18	ADRI0609	Adri0609 Dog Ige e
2	87	89.7	18	ADRI0610	Adri0610 Cat Ige e
3	55	56.7	18	ADRI0612	Adri0612 Sheep Ige
4	37	38.1	15	ADCS6890	Adcs6890 Peptide f
5	34	35.1	15	ADCS6890	Adcs6890 Horse imm
6	34	35.1	18	ADRI0611	Adri0611 Horse Ige
7	32.5	33.5	15	ADW78189	Adw78189 Human met
8	32	33.0	9	AAU76520	Aau76520 Anti-Inte
9	32	33.0	9	AAE15818	Aae15818 Human mab
10	32	33.0	9	AAE76312	Aae76312 Prostate
11	32	33.0	11	ADT40399	Adt40399 hSARS vir
12	32	33.0	11	ADT40399	Adt40399 hSARS vir
13	32	33.0	11	ADT79816	Adt79816 SARS vir
14	32	33.0	11	ADT79816	Adt79816 SARS vir
15	32	33.0	12	AAAS2787	Aaas2787 CCR5-bind
16	32	33.0	12	AAAS2787	Aaas2787 CCR5-bind
17	32	33.0	15	ADVI3048	Advi3048 Human pho
18	32	33.0	15	ADVI3048	Advi3048 Human pho
19	32	33.0	15	AAV65747	Aav65747 Breast ca
20	32	33.0	15	ADN64911	Adn64911 HLA bindi
21	32	33.0	14	ADN64911	Adn64911 HLA bindi
22	32	33.0	14	ADN64911	Adn64911 HLA bindi
23	32	33.0	14	ADN64911	Adn64911 HLA bindi
24	32	33.0	14	ADN64911	Adn64911 HLA bindi
25	32	33.0	14	ADN64911	Adn64911 HLA bindi
26	32	33.0	14	ADN64911	Adn64911 HLA bindi
27	32	33.0	14	ADN64911	Adn64911 HLA bindi
28	32	33.0	14	ADN64911	Adn64911 HLA bindi
29	32	33.0	14	ADN64911	Adn64911 HLA bindi
30	32	33.0	14	ADN64911	Adn64911 HLA bindi
31	32	33.0	14	ADN64911	Adn64911 HLA bindi
32	32	33.0	14	ADN64911	Adn64911 HLA bindi
33	32	33.0	14	ADN64911	Adn64911 HLA bindi
34	32	33.0	14	ADN64911	Adn64911 HLA bindi
35	32	33.0	14	ADN64911	Adn64911 HLA bindi
36	32	33.0	14	ADN64911	Adn64911 HLA bindi
37	32	33.0	14	ADN64911	Adn64911 HLA bindi
38	32	33.0	14	ADN64911	Adn64911 HLA bindi
39	32	33.0	14	ADN64911	Adn64911 HLA bindi
40	32	33.0	14	ADN64911	Adn64911 HLA bindi
41	32	33.0	14	ADN64911	Adn64911 HLA bindi
42	32	33.0	14	ADN64911	Adn64911 HLA bindi
43	32	33.0	14	ADN64911	Adn64911 HLA bindi
44	32	33.0	14	ADN64911	Adn64911 HLA bindi
45	32	33.0	14	ADN64911	Adn64911 HLA bindi

24	30	30.9	10	7	ADD94544	Add94544 Human SIM
25	30	30.9	14	3	AB39162	Ab39162 Human sec
26	30	30.9	14	3	AB39163	Ab39163 Human sec
27	30	30.9	16	2	AAR53562	Aar53562 Birch pol
28	30	30.9	16	8	ADQ90450	Adq90450 RANTES re
29	30	30.9	17	2	AAR95159	Aar95159 bcl-x(L)/
30	29	29.9	9	2	AAW24775	Aaw24775 Human imm
31	29	29.9	9	2	AAW80144	Aaw80144 Light cha
32	29	29.9	9	2	AAW80142	Aaw80142 Light cha
33	29	29.9	9	2	AAW80142	Aaw80142 Light cha
34	29	29.9	9	2	AAW80142	Aaw80142 Light cha
35	29	29.9	9	2	AAW80142	Aaw80142 Light cha
36	29	29.9	9	2	AAW80142	Aaw80142 Light cha
37	29	29.9	9	2	AAW80142	Aaw80142 Light cha
38	29	29.9	9	2	AAW80142	Aaw80142 Light cha
39	29	29.9	9	2	AAW80142	Aaw80142 Light cha
40	29	29.9	9	2	AAW80142	Aaw80142 Light cha
41	29	29.9	9	2	AAW80142	Aaw80142 Light cha
42	29	29.9	9	2	AAW80142	Aaw80142 Light cha
43	29	29.9	9	2	AAW80142	Aaw80142 Light cha
44	29	29.9	9	2	AAW80142	Aaw80142 Light cha
45	29	29.9	9	2	AAW80142	Aaw80142 Light cha

ALIGNMENTS

RESULT 1
ID ADRI0609 standard; peptide; 18 AA.
XX
AC ADRI0609;
XX
DT 21-OCT-2004 (first entry)
XX
DE Dog Ige epitope recognised by monoclonal antibody 3.76, SEQ ID 9.
XX
KM Antiaesthetic; Antiallergic; Immunosuppressive; Ige; dog; asthma;
XX anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody.
XX
OS Canis familiaris.
XX
PN WO2004065936-A2.
XX
PD 05-AUG-2004.
XX
PF 15-JAN-2004; 2004WO-US003566.
XX
PR 16-JAN-2003; 2003US-044072P.
XX
PA (UNIC-) UNIV NORTH CAROLINA STATE.
XX
PI Hammerberg B;
XX
DR WPI; 2004-593545/57.
XX
PT Novel antibody that specifically binds to mammalian Ige epitope, useful
XX for testing an allergen reactivity of Ige sample, detecting mammalian Ige
XX or treating asthma or anaphylactic shock.
XX
PS Example 6; Page 9; 14pp; English.
XX
XX The present invention relates to a novel monoclonal antibody (I) that
XX specifically binds to a mammalian Ige epitope, where the epitope is
XX between amino acids 145-166 or 356-374 of mammalian Ige, e.g. dog Ige.
XX (II) is useful for testing an allergen reactivity of an Ige sample.
XX allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
XX and corn allergens. The sample is a biological sample collected from a
XX dog, cat or horse. (I) is also useful for detecting mammalian Ige and for
XX treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
XX antibodies recognise epitopes on canine Ige corresponding to amino acid
XX residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the
XX canine Ige epsilon-chain. Recognition of epsilon-chains from Ige from

CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with
 CC either pig or human epsilon-chains of IGE.

XX Sequence 18 AA;

Query Match 100.0%; Score 97; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 6.5e-09;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGQKATNIFPYTAGTK 18
 |||||
 1 VDGQKATNIFPYTAGTK 18

RESULT 2
 ADRI0610
 ID ADRI0610 standard; peptide; 18 AA.

XX ADRI0610;

DT 21-OCT-2004 (first entry)

DE Cat IGE epitope recognised by monoclonal antibody 3.76, SEQ ID 10.

KW Antiasthmatic; Antiallergic; Immunosuppressive; IGE; dog; asthma;
 KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
 cat.

XX Fells catus.

XX WO2004065936-A2.

XX 05-AUG-2004.

XX 15-JAN-2004; 2004WO-US003566.

XX 16-JAN-2003; 2003US-0440472P.

XX (UYN(-) UNIV NORTH CAROLINA STATE.

XX Hammerberg B;

DR WPI; 2004-593545/57.

PT Novel antibody that specifically binds to mammalian IGE epitope, useful
 PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE
 PT or treating asthma or anaphylactic shock.

PS Example 6; Page 9; 14pp; English.

CC The present invention relates to a novel monoclonal antibody (I) that
 CC specifically binds to a mammalian IGE epitope, where the epitope is
 CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
 CC (I) is useful for testing an allergen reactivity of an IGE sample. The
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
 CC and corn allergens. The sample is a biological sample collected from a
 CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
 CC antibodies recognise epitopes on canine IGE corresponding to amino acid
 CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the
 CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with
 CC either pig or human epsilon-chains of IGE. The present sequence is the
 CC cat IGE 3.76 recognition site.

XX Sequence 18 AA;

Query Match 89.7%; Score 87; DB 8; Length 18;
 Best Local Similarity 100.0%; Pred. No. 3.1e-07;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VDGQKATNIFPYTAG 16
 |||||
 1 VDGQKATNIFPYTAG 16

RESULT 3
 ADRI0612
 ID ADRI0612 standard; peptide; 18 AA.

XX ADRI0612;

DT 21-OCT-2004 (first entry)

DE Sheep IGE epitope recognised by monoclonal antibody 3.76, SEQ ID 12.

KW Antiasthmatic; Antiallergic; Immunosuppressive; IGE; dog; asthma;
 KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
 sheep.

XX Ovis aries.

XX WO2004065936-A2.

XX 05-AUG-2004.

XX 15-JAN-2004; 2004WO-US003566.

XX 16-JAN-2003; 2003US-0440472P.

XX (UYN(-) UNIV NORTH CAROLINA STATE.

XX Hammerberg B;

DR WPI; 2004-593545/57.

PT Novel antibody that specifically binds to mammalian IGE epitope, useful
 PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE
 PT or treating asthma or anaphylactic shock.

PS Example 6; Page 9; 14pp; English.

CC The present invention relates to a novel monoclonal antibody (I) that
 CC specifically binds to a mammalian IGE epitope, where the epitope is
 CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
 CC (I) is useful for testing an allergen reactivity of an IGE sample. The
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
 CC and corn allergens. The sample is a biological sample collected from a
 CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
 CC antibodies recognise epitopes on canine IGE corresponding to amino acid
 CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the
 CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with
 CC either pig or human epsilon-chains of IGE. The present sequence is the
 CC sheep IGE 3.76 recognition site.

XX Sequence 18 AA;

Query Match 56.7%; Score 55; DB 8; Length 18;
 Best Local Similarity 66.7%; Pred. No. 0.071;
 Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 VDGQKATNIFPYTAG 15
 |||||
 1 VDGQEDRWLFSTYAP 15

RESULT 4
 ADC56890

```

ID  ADC56890 standard; peptide; 15 AA.
XX
XX  ADC56890;
AC
XX  18-DEC-2003 (first entry)
XX
XX  Peptide fragment Seq ID7 related to human protein 36-41.
DE
XX  human; protein 36-41; arrhythmia; asthma; dementia.
XX
XX  Homo sapiens.
OS
XX  CN1382718-A.
XX
XX  04-DEC-2002.
PD
XX  26-APR-2001; 2001CN-00112751.
XX
XX  26-APR-2001; 2001CN-00112751.
XX
XX  26-APR-2001; 2001CN-00112751.
PR
XX  (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
XX  Mao Y, Xie Y;
PI
XX  WPI; 2003-269480/27.
XX
XX  New human macroprotein-36-41, encoding polynucleotide, antagonist and
PT  recombinant production, useful for treating dementia, arrhythmia, asthma
PT  and digestive ulcers.
XX
XX  Example 6; SEQ ID NO 7; 33pp; Chinese.
XX
XX  This invention relates to a novel protein, human protein 36-41, and the
CC  DNA sequence encoding it. The protein of the invention may be useful for
CC  the treatment of diseases such as arrhythmia, asthma and dementia. The
CC  present sequence is the amino acid sequence of a peptide fragment of
CC  human protein 36-41 which was used in the exemplification of the
CC  invention.
XX
XX  Sequence 15 AA;
SQ
XX
XX  Query Match 38.1%; Score 37; DB 7; Length 15;
XX  Best Local Similarity 40.0%; Pred. No. 60;
XX  Matches 6; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 1 VDGQKATNIFPYTAP 15
   :|||:||||:
Db 1 MDGKMQPNSFPWQSP 15

RESULT 5
AD64569
ID  AD64569 standard; peptide; 15 AA.
XX
XX  AD64569;
AC
XX  18-DEC-2003 (first entry)
XX
XX  Horse immunoglobulin E, IgE, heavy chain immunogenic peptide P5.
DE
XX  Horse; immunoglobulin E; IgE; heavy chain; immunogen; allergy.
XX
XX  Equus caballus.
OS
XX  US2003087314-A1.
XX
XX  08-MAY-2003.
PD
XX  08-NOV-2001; 2001US-00052788.
XX
XX  08-NOV-2001; 2001US-00052788.
XX
XX  (REGC ) UNIV CALIFORNIA.
PA

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XX  Gershwin LJ, Pettigrew HD, Kalina WV;
PI  WPI; 2003-765437/72.
XX
XX  Immunogenic composition comprising an isolated equine immunoglobulin E
PT  polypeptide that induces production of antibodies which specifically bind
PT  to equine immunoglobulin E.
XX
XX  Example 1; Page 8; 14pp; English.
XX
XX  The invention relates to an immunogenic composition comprising an
CC  isolated polypeptide having an amino acid sequence that is at least 80%
CC  identical to 6 (S1-S6), 15 amino acid peptide sequences derived from
CC  equine immunoglobulin E (the composition induces production of an
CC  antibody that specifically binds to equine immunoglobulin (Ig)E), the six
CC  polypeptides are not explicitly identified in the specification. Also
CC  included are a composition comprising an antibody that specifically binds
CC  to a polypeptide at least 80% identical to (S1)-(S6), an antibody that
CC  specifically binds to equine IgE made by the process of immunising an
CC  animal with a polypeptide at least 80% identical to (S1)-(S6), making an
CC  antibody that specifically binds to equine IgE (involving immunising an
CC  animal with a composition further comprising an isolated polypeptide (the
CC  amino acid sequence of the polypeptide is at least 80% identical to (S1)-
CC  (S6)), and collecting antiserum from the animal) and a kit for detection
CC  of equine IgE in a biological sample comprising the antibody and means
CC  for detecting specific binding of the antibody to equine IgE. The
CC  antibody is useful for detecting equine IgE protein in a biological
CC  sample (serum) which involves contacting the sample with the antibody,
CC  thus forming an antigen/antibody complex, and detecting the presence or
CC  absence of the antigen/antibody complex. The antibody and antigen are
CC  immobilised on a solid surface. The antibody is labelled such that the
CC  complex can be detected. The complex is detected using a second labelled
CC  antibody. The peptides are useful for generating antibodies specific for
CC  IgE which can serve as a diagnostic test for allergy. The present
CC  sequence is a Horse immunoglobulin E, IgE, heavy chain immunogenic
XX  peptide from the middle portion of the C2 region.
XX
XX  Sequence 15 AA;
SQ
XX
XX  Query Match 35.1%; Score 34; DB 7; Length 15;
XX  Best Local Similarity 54.5%; Pred. No. 1.9e+02;
XX  Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 VDGQKATNIFP 11
   :|||:|
Db 2 IDGKRVDEQFP 12

RESULT 6
ADR10611
ID  ADR10611 standard; peptide; 18 AA.
XX
XX  ADR10611;
AC
XX  21-OCT-2004 (first entry)
XX
XX  Horse IgE epitope recognised by monoclonal antibody 3.76, SEQ ID 11.
DE
XX  Antiasthmatic; Antiallergic; Immunosuppressive; IgE; dog; asthma;
XX  anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
XX  horse.
XX
XX  Equus caballus.
OS
XX  WO2004065936-A2.
XX
XX  05-AUG-2004.
PD
XX  15-JAN-2004; 2004WO-US003566.
XX
XX  16-JAN-2003; 2003US-0440472P.
XX

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PA (UYNC-) UNIV NORTH CAROLINA STATE.
 XX
 XX Hammerberg B;
 XX
 DR WPI; 2004-593545/57.
 XX
 XX Novel antibody that specifically binds to mammalian Igs epitope, useful
 PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE
 PT or treating asthma or anaphylactic shock.
 XX
 XX Example 6; Page 9; 14pp; English.
 XX
 XX The present invention relates to a novel monoclonal antibody (I) that
 CC specifically binds to a mammalian IGE epitope, where the epitope is
 CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
 CC (I) is useful for testing an allergen reactivity of an IGE sample. The
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
 CC and corn allergens. The sample is a biological sample collected from a
 CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
 CC antibodies recognise epitopes on canine IGE corresponding to amino acid
 CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the
 CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with
 CC either pig or human epsilon-chains of IGE. The present sequence is the
 CC horse IGE 3.76 recognition site.
 XX
 XX Sequence 18 AA;
 XX
 SQ
 Query Match 35.1%; Score 34; DB 8; Length 18;
 Best Local Similarity 54.5%; Pred. No. 2.3e+02;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 Oy 1 VDGKATNIFP 11
 :||| |
 1 IDGKVDQF 11
 Db
 RESULT 7
 ADW78189
 ID ADW78189 standard; peptide; 15 AA.
 XX
 AC ADM78189;
 XX
 DT 07-APR-2005 (first entry)
 XX
 DE Human metabolic therapy target peptide PAGT.
 XX
 XX DEF domain: MAP kinase; cytosolic; cardiovascular-gen.; cardiac;
 KW vasoactive; hypotensive; antiarteriosclerotic; antiinflammatory;
 KW antiallergic; immunosuppressive; antibacterial; antitumor;
 KW dermatological; antidiabetic; gastrointestinal-gen.; antidiabetic;
 KW thrombolytic; neuroprotective; ophthalmological; antineoplastic;
 KW antipyretic; uropathic; antiproliferative; hepatocytic; antineoplastic;
 KW muscular-gen.; thymic; antihypertensive; hepatocytic; nephrotoxic;
 KW hepatocytic; virucide; anti-HIV; anabolic; hypertensive; anorectic;
 KW endocrine-gen.; neuroleptic; nootropic; antiparkinsonian; anticonvulsant;
 KW antidepressant; antidiabetic; sedative; hypnotic; CNS-gen.;
 KW antineoplastic; cancer; cardiovascular disease; inflammation;
 KW metabolic disorder; neuropathy; sleep disorder.
 XX
 XX Homo sapiens.
 OS
 XX WO2005007090-A2.
 FN
 XX 27-JAN-2005.
 PD
 XX 02-JUL-2004; 2004WO-US021514.
 XX
 XX 03-JUL-2003; 2003US-0484761P.
 PR
 XX

PA (HARD) HARVARD COLLEGE.
 XX
 XX Blenis J, Murphy LO;
 XX
 DR WPI; 2005-112720/12.
 XX
 XX Identification of compound for treating e.g. cancer by culturing cells
 PT expressing target protein in the presence of growth factor, cytokine,
 PT tumor promoter or oncogene and assessing binding after contacting with
 PT the compound.
 XX
 XX Claim 14; Page 64; 104pp; English.
 XX
 XX The invention relates to a novel method for the identification of a
 CC therapeutic compound. The method involves providing test cells that
 CC express a target protein containing a DEF domain and MAP kinase;
 CC culturing the cells in the presence of growth factor, cytokine, tumor
 CC promoter or oncogene; contacting the cells with a candidate compound; and
 CC assessing the binding of the MAP kinase to the DEF domain relative to the
 CC binding in the absence of the candidate compound. The invention further
 CC comprises a method for the identification of a therapeutic compound; a
 CC method for treatment of cancer, which involves administering a compound
 CC that inhibits the binding of a MAP kinase to the DEF domain of a target
 CC protein; and an antibody that specifically binds to phospho-T-325 C-Fos
 CC (preferably polyclonal or monoclonal). The novel therapeutic compounds
 CC have the following activities: cytosolic; cardiovascular-gen.; cardiac;
 CC vasoactive; hypotensive; antiarteriosclerotic; antiinflammatory;
 CC antiallergic; immunosuppressive; antibacterial; antitumor;
 CC dermatological; antidiabetic; gastrointestinal-gen.; antitumor;
 CC thrombolytic; neuroprotective; ophthalmological; antineoplastic;
 CC antipyretic; uropathic; antiproliferative; hepatocytic; antineoplastic;
 CC -gen.; thymic; antihypertensive; hepatocytic; nephrotoxic;
 CC hepatocytic; virucide; anti-HIV; anabolic; hypertensive; anorectic;
 CC endocrine-gen.; neuroleptic; nootropic; antiparkinsonian; anticonvulsant;
 CC antidepressant; antidiabetic; sedative; hypnotic; CNS-gen.; and
 CC antineoplastic. The therapeutic compound may be used in the treatment
 CC of: cancer, cardiovascular disorders, inflammatory disorders, metabolic
 CC disorders, neuropathy or a behavioural disorder, and a sleep disorder.
 CC This sequence represents a metabolic therapy target peptide of the
 CC invention.
 XX
 XX Sequence 15 AA;
 XX
 SQ
 Query Match 33.5%; Score 32.5; DB 9; Length 15;
 Best Local Similarity 66.7%; Pred. No. 3.4e+02;
 Matches 8; Conservative 0; Mismatches 1; Indels 3; Gaps 1;
 Oy 5 KATNIFPYTAPG 16
 :||| |
 1 KAT--PYTFPG 9
 Db
 RESULT 8
 AAU76520
 ID AAU76520 standard; peptide; 9 AA.
 XX
 AC AAU76520;
 XX
 DT 05-JUN-2002 (first entry)
 XX
 DE Anti-Interleukin-12 (IL-12) antibody CDR3 light chain.
 XX
 XX Human; antibody; anti-interleukin-12; CDR; light chain; circularity;
 KW complementarity determining region; neuroprotective; antiproliferative;
 KW immunostimulant; cytosolic; anti-microbial; psoriasis; infection;
 KW multiple sclerosis; immune disorder; cardiovascular; malignant disease;
 KW neurological disorder.
 XX
 XX Homo sapiens.
 OS
 XX WO200212500-A2.
 FN
 XX 14-FEB-2002.
 PD

XX 07-AUG-2001; 2001WO-US024720.
 PF 07-AUG-2000; 2000US-0223358P.
 XX 29-SEP-2000; 2000US-0236827P.
 PR 01-AUG-2001; 2001US-00920262.
 XX (CENZ) CENTOCOR INC.
 PA
 XX Giles-Komar J, Knight DM, Peritt D, Scallion B, Shealy D;
 P1 WPI; 2002-257482/30.
 XX
 DR New mammalian anti-IL-12 antibodies, useful for diagnosing or treating IL
 XX -12 related conditions, e.g. psoriasis or multiple sclerosis, as well as
 PT other for treating immune, infectious, malignant or neurological
 PT disorders.
 XX
 PS Claim 41; Page 93; 96pp; English.
 XX
 CC The invention relates to novel isolated mammalian anti-interleukin-12 (IL
 CC -12) antibodies. The antibodies comprise at least one complementarily
 CC determining region (CDR) of a heavy or light chain, a heavy chain or
 CC light chain variable region, or a heavy chain or light chain constant
 CC region. The anti-IL-12 antibodies are useful in methods for diagnosing or
 CC treating IL-12 related conditions, e.g. psoriasis or multiple sclerosis.
 CC The antibodies are also useful for treating immune, cardiovascular,
 CC infectious, malignant or neurological disorders or diseases. The present
 CC sequence represents the amino acid sequence of human anti-interleukin-12
 CC (IL-12) antibody CDR3 light chain
 XX
 SO Sequence 9 AA;

Query Match 33.0%; Score 32; DB 5; Length 9;
 Best Local Similarity 83.3%; Pred. No. 2.1e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 8 NIPYPT 13
 ||:||||
 Db 4 NIPYPT 9

RESULT 9
 AAE15818
 ID AAE15818 standard; peptide; 9 AA.
 XX
 AC AAE15818;
 XX

DT 26-MAR-2002 (first entry)
 XX

DE Human mAb 12B1 VK complementarily determining region (CDR) #3.
 XX

XX Human; sialoadhesin factor-3; SAF-3; therapy; cancer; inflammation;
 KW autoimmunity; allergy; asthma; infection; central nervous system; CNS;
 KW rheumatoid arthritis; multiple sclerosis; stem cell mobilisation; AIDS;
 KW haematopoietic development; anaemia; chemoprotective agent; cytostatic;
 KW immunoglobulin; complementarity determining region; CDR; protozoacide;
 KW antineoplastic; immunosuppressive; anti-HIV; antibacterial; virucide;
 KW fungicide; neuroprotective; light chain variable region; VK; mAb;
 KW monoclonal antibody.
 XX
 OS Homo sapiens.
 XX
 PN WO200190193-A1.
 XX
 PD 29-NOV-2001.
 XX
 PF 24-MAY-2001; 2001WO-US016864.
 XX
 PR 24-MAY-2000; 2000US-00577930.
 XX
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PA (SMIK) SMITHKLINE BEECHAM PLC.

XX Abrahamsen JA, Kikly KK;
 PI WPI; 2002-083094/11.
 DR
 XX Novel monoclonal antibody that binds to human sialoadhesin factor-3 for
 PT treating or preventing cancer, inflammation, autoimmunity, allergy,
 PT asthma, rheumatoid arthritis, multiple sclerosis, AIDS and infections.
 XX
 PS Claim 13; Page 67; 69pp; English.
 XX

XX The invention relates to monoclonal antibodies that bind to human
 CC sialoadhesin factor-3 (SAF-3). SAF-3 antibody is useful for treating or
 CC preventing cancer, inflammation, autoimmunity, allergy, asthma, central
 CC nervous system (CNS) inflammation, rheumatoid arthritis, multiple
 CC sclerosis, AIDS and bacterial, fungal, protozoan and viral infections and
 CC for modulating an immune response in a mammal, where the immune response
 CC is downregulated or enhanced. SAF-3 antibody is useful as diagnostic and
 CC therapeutic reagents, to subcharacterise cell populations during
 CC haematopoietic development, to treat anaemia, as a diagnostic marker to
 CC distinguish between different forms of cancer, to purge bone marrow ex
 CC vivo of cancer cells expressing SAF-3, as a tool to aid in the ex vivo
 CC expansion (proliferation and/or differentiation) of haematopoietic
 CC progenitor cells expressing SAF-3, as a stimulus in vivo for stem cell
 CC mobilisation into the periphery and as an vivo chemoprotective agent.
 CC Protein comprising immunoglobulin complementarily determining region
 CC (CDR) of SAF-3 antibody and its nucleic acid is useful to configure
 CC screening methods for detecting the effect of added compounds on the
 CC production of mRNA and polypeptide in cells. The present sequence is
 CC complementarily determining region of human monoclonal antibody (mAb)
 CC 12B1 light chain variable region (VK), which binds to SAF-3
 XX
 SO Sequence 9 AA;

Query Match 33.0%; Score 32; DB 5; Length 9;
 Best Local Similarity 83.3%; Pred. No. 2.1e+06;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 8 NIPYPT 13
 ||:||||
 Db 4 NIPYPT 9

RESULT 10
 AEF76312
 ID AEF76312 standard; protein; 9 AA.
 XX
 AC AEF76312;
 XX

DT 20-APR-2006 (first entry)
 XX

DE Prostate cancer cell antibody light chain CDR3 SEQ ID NO:65.
 XX

XX antibody; prostate tumor; cytostatic; andrology; genitourinary disease;
 KW neoplasm; antibody identification; antibody therapy; light chain.
 KW
 XX Mus musculus.
 OS
 PN WO2006017173-A1.
 XX
 PD 16-FEB-2006.
 XX
 PF 08-JUL-2005; 2005WO-US024260.
 XX
 PR 10-JUL-2004; 2004US-0586811P.
 XX
 PA (ALEX-) ALEXION PHARM INC.
 XX
 PI Bowdish KS, Xin H, Yanciri F, Siva A;
 XX
 DR WPI; 2006-173528/18.
 XX
 PT New antibody that binds to a prostate cancer cell, useful for detecting

PT	cancerous cells in vivo, for killing or ablating prostate cancer cells in
PT	vivo, and for delivering a variety of cytotoxic drugs.
XX	
PS	Claim 16; SEQ ID NO 65; 48bp; English.
XX	
CC	The invention relates to an antibody (I) that binds to a prostate cancer
CC	cell. Also described are the following: identifying (M1) antibodies
CC	specific to cancer cells; generating a phage displayed antibody library
CC	using cells collected from subjects immunized with cancer cells; removing
CC	members of the library that bind to human red blood cells to generate a
CC	sub-library, and recovering from the sub-library members that display
CC	antibodies that bind to the cancer cell; or contacting cancer cells with
CC	a hapten, generating a phage displayed antibody library using cells
CC	collected from subjects immunized with cancer cells, removing members of
CC	the library that bind to human red blood cells to generate a sub-library,
CC	and recovering from the sub-library members that display antibodies that
CC	bind to the cancer cell; an isolated nucleic acid (II) encoding (I); an
CC	expression vector (III) comprising (II); a host cell (IV) transfected
CC	with (III); and an antibody that binds to Cdcpl. (M1) is useful for
CC	identifying antibodies specific to cancer cells. (I) is useful as a
CC	therapeutic for cancer, for detecting cancerous cells in vivo, for
CC	killing or ablating cancerous cells in vivo (preferably prostate cancer
CC	cells), and for delivering a variety of cytotoxic drugs including
CC	therapeutic drugs, a compound emitting radiation, molecules of plants,
CC	fungal or bacterial origin, biological proteins, and their mixtures. The
CC	present sequence represents prostate cancer cell antibody light chain
CC	CDR3 SEQ ID NO:65.
XX	
SQ	Sequence 9 AA;
	Query Match 33.0%; Score 32; DB 10; Length 9;
	Best Local Similarity 83.3%; Pred. NO. 2.1e+06;
	Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0
QY	8 NIEPYT 13
	:
Db	4 NIEPYT 9
RESULT 11	
ID	ADT40399 standard; peptide; 11 AA.
XX	
AC	ADT40399;
XX	
DT	30-DEC-2004 (first entry)
XX	
DE	hSARS virus peptide, SEQ ID 1367.
XX	
KM	Virucide; Severe Acute Respiratory Syndrome; SARS; vaccine.
OS	
XX	SARS coronavirus.
XX	
PN	WO2004085650-A1.
XX	
PD	07-OCT-2004.
XX	
PF	24-MAR-2004; 2004WO-CN000246.
XX	
PR	24-MAR-2003; 2003US-0457031P.
PR	26-MAR-2003; 2003US-0457730P.
PR	02-APR-2003; 2003US-0459931P.
PR	03-APR-2003; 2003US-0460357P.
PR	08-APR-2003; 2003US-0461265P.
PR	14-APR-2003; 2003US-0462805P.
PR	23-APR-2003; 2003US-0464886P.
PR	25-APR-2003; 2003US-0465738P.
PR	14-MAY-2003; 2003US-0470935P.
XX	
PA	(UHK-) UNITV HONG KONG.
XX	
PI	Chan K, Guan Y, Nicholas JM, Petris JSM, Poon L, Yuen K;
	Leung FC;

[illegible]

PA (UYHK-) UNIV HONG KONG.
XX
PI Chan K, Guan Y, Nicholls JM, Peiris JSM, Poon L, Yuen K,
XX
DR WPI; 2004-737292/72.
XX
PT New isolated nucleic acid molecule useful for detecting, treating,
PT ameliorating, or preventing the virus causing severe acute respiratory
PT syndrome in humans using a real-time quantitative polymerase chain
PT reaction assay.
XX
PS Example; SEQ ID NO 1387; 183pp; English.
XX
CC The invention relates to an isolated nucleic acid molecule consisting
CC essentially of, and/or hybridizes under stringent conditions to a fully
CC defined nucleotide sequence of 16-25 base pairs (bp); SEQ ID NO: 2471-
CC 2476), or its complement. The methods and compositions of the present
CC invention are useful for the detection of the virus causing Severe Acute
CC Respiratory Syndrome (SARS) in humans using a real-time quantitative
CC polymerase chain reaction (PCR) assay. They can also be used in treating,
CC ameliorating, managing or preventing SARS. This sequence corresponds to a
CC partial SARS protein sequence from the complementary reading frame 1.
XX
SQ Sequence 11 AA;

Query Match 33.0%; Score 32; DB 8; Length 11;
Best Local Similarity 54.5%; Pred. No. 3e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 GOKATNIFPYT 13
Db 1 GOSOSNIPPT 11
		:				
		:				
		:				

RESULT 13
ADT37929
ID ADT37929 standard; peptide; 11 AA.
XX
AC ADT37929;
XX
DT 30-DEC-2004 (first entry)
XX
DE hSARS virus peptide, SEQ ID 1387.
XX
KM Virucide; Severe Acute Respiratory Syndrome; SARS; vaccine.
XX
OS SARS coronavirus.
XX
PN WO2004085633-A1.
XX
PD 07-OCT-2004.
XX
PE 24-MAR-2004; 2004WO-CN000248.
XX
PR 24-MAR-2003; 2003US-0457031P.
PR 26-MAR-2003; 2003US-0457730P.
PR 02-APR-2003; 2003US-0459931P.
PR 03-APR-2003; 2003US-0460357P.
PR 08-APR-2003; 2003US-0461265P.
PR 14-APR-2003; 2003US-0462805P.
PR 23-APR-2003; 2003US-0464886P.
XX
PA (UYHK-) UNIV HONG KONG.
XX
PI Chan K, Guan Y, Nicholls JM, Peiris JSM, Poon L, Yuen K;
XX
DR WPI; 2004-728736/71.
XX
PT New isolated human severe acute respiratory syndrome (hSARS) virus,
PT useful as vaccine for diagnosing or treating SARS or in clinical and
PT scientific research applications.
XX

PS Example; SEQ ID NO 1387; 176pp; English.
XX
CC The present invention relates to novel human Severe Acute Respiratory
CC Syndrome (hSARS) viral nucleic acid and protein sequences derived from a
CC hSARS virus having China Center for Type Culture Collection Deposit
CC Accession No. CCRCC-V200303. The hSARS virus, nucleic acid and protein
CC sequences are useful as vaccines for diagnosing or treating SARS. They
CC are also useful in clinical and scientific research applications. The
CC hSARS virus genome (ADT36557) was obtained and the amino acid sequences
CC of all three reading frames were deduced from the complementary strand.
CC ADT37650 is the full-length protein encoded by the first reading frame of
CC the complementary strand and ADT37651-ADT38131 are the peptides from the
CC first reading frame protein. ADT38132 is the full-length protein encoded
CC by the second reading frame of the complementary strand and ADT38133-
CC ADT38506 are the peptides from the second reading frame protein. ADT38507
CC is the full-length protein encoded by the third reading frame of the
CC complementary strand and ADT38508-ADT39012 are the peptides from the
CC third reading frame protein.
XX
SQ Sequence 11 AA;

Query Match 33.0%; Score 32; DB 8; Length 11;
Best Local Similarity 54.5%; Pred. No. 3e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 GOKATNIFPYT 13
Db 1 GOSOSNIPPT 11
		:				
		:				
		:				

RESULT 14
AAMS2787
ID AAMS2787 standard; peptide; 12 AA.
XX
AC AAMS2787;
XX
DT 22-FEB-2002 (first entry)
XX
DE CCR5-binding phage display peptide #4.
XX
KM CCR5 binding peptide; CC chemokine receptor 5; human; HIV infection;
KM human immunodeficiency virus; AIDS; acquired immunodeficiency syndrome;
KM drug screening; identification; phage display library.
XX
OS Synthetic.
XX
PN WO200171346-A2.
XX
PD 27-SEP-2001.
XX
PE 21-MAR-2001; 2001WO-US0009155.
XX
PR 21-MAR-2000; 2000US-0190946P.
PR 21-MAR-2000; 2000US-0190966P.
PR 21-MAR-2000; 2000US-0191299P.
PR 20-MAR-2001; 2001US-00813448.
PR 20-MAR-2001; 2001US-00813651.
PR 20-MAR-2001; 2001US-00813653.
XX
PA (CONS-) CONSENSUS PHARM INC.
XX
PI Nestor JJ, Wilson CJ, See RH, Tan Hehir CA;
XX
DR WPI; 2002-010610/01.
XX
PT Identifying CC chemokine receptor 5 binding compound for treating AIDS,
PT comprises binding a molecule from library to a molecule having binding
PT property corresponding to CCR5 and identifying bound molecule.
XX
PS Claim 20; Page 33; 50pp; English.
XX
CC The invention relates to a method for identifying a binding compound for
CC CC chemokine receptor 5 (CCR5). The method involves screening a library

CC of test molecules (particularly peptides) with immobilised CCR5, and then
CC identifying those molecules which bind. The invention also relates to
CC CCR5-binding molecules identified using the method of the invention,
CC methods for identifying consensus motifs for CCR5-binding peptides, a
CC transfer vector encoding tagged CCR5, a computer-aided methods for
CC determining the relative binding affinity of a test molecule to CCR5 and
CC a computer aided drug screening assay that utilises the three-dimensional
CC structure of CCR5. Compounds identified using the methods of the
CC invention are useful for treating or preventing HIV (human
CC immunodeficiency virus) infection or AIDS (acquired immunodeficiency
CC syndrome) in a patient. The methods of the invention may also be used to
CC identify agonists or antagonists of the interaction of CCR5 with its
CC natural ligand, and to determine a binding motif for CCR5. Sequences
CC AAM52784-AAM52805 and AAM52814 represent specifically claimed CCR5-
CC binding peptides identified using methods of the invention
XX
SQ Sequence 12 AA;
Query Match 33.0%; Score 32; DB 5; Length 12;
Best Local Similarity 62.5%; Pred. No. 3.3e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 10 PPTAPGT 17
:|:|:|
4 YPTGAPRT 11
DB
RESULT 15
ADV13048
ID ADV13048 standard; peptide; 12 AA.
XX
AC ADV13048;
XX
DT 10-MAR-2005 (first entry)
XX
DE Human phosphorylated peptide from phosphoprotein #986.
XX
KW Alzheimer disease; neuroprotective; nootropic; degeneration; tumor;
KW neoplasm; neurological disease; phosphorylation; protein sequencing;
KW phosphoprotein.
XX
OS Homo sapiens.
XX
PN W02004108948-A2.
XX
PD 16-DEC-2004.
XX
PF 04-JUN-2004; 2004WO-US017613.
XX
PR 04-JUN-2003; 2003US-0476010P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI GYGI SP;
XX
DR WPI; 2005-031720/03.
XX
PT Characterizing phosphorylated polypeptides in a sample comprises
PT digesting the polypeptides with a protease thus generating test peptides,
PT and collecting a fraction of test peptides that enriched for positively
PT charged peptides.
XX
PS Claim 16; Page 79; 123pp; English.
XX
CC The invention relates to characterizing phosphorylated polypeptides in a
CC sample comprising digesting the polypeptides with a protease thus
CC generating test peptides, and collecting a fraction of test peptides that
CC enriched for positively charged peptides. Also included are a method
CC (comprising determining the presence, absence or level of one ore more
CC phosphorylated peptides as identified above in cells having a cell state
CC and determining the degree of correlation between the presence, absence
CC or level of phosphorylated polypeptide with the cell state), an isolated
CC peptide of 5-50 amino acids comprising an amino acid sequence that is a

CC subsequence of any of the protein sequences given in the specification
CC (and which comprise a phosphorylation site within the subsequence), an
CC isolated polypeptide selected from any of the polypeptides listed in the
CC specification and is modified at a modification site, an isolated peptide
CC comprising a mass spectral peak signatures, a method for identifying a
CC treatment that modulates phosphorylation of an amino acid in a target
CC polypeptide, a method for generating a peptide standard, a pair of
CC peptide standards comprising the peptide obtained (where the peptide is
CC phosphorylated and a corresponding peptide comprising an identical amino
CC acid sequence but which is not phosphorylated), a system (comprising a
CC computer memory comprising data files storing information relating to the
CC identifying characteristics of positively charged peptides, and a data
CC analysis module capable of executing instructions for organizing and/or
CC searching the data files), a computer program product (comprising data
CC relating to the identifying characteristics of positively charged
CC peptides and comprising instructions for organizing and/or searching the
CC data), and a method for identifying N-terminal peptides in a sample. The
CC method is useful for characterizing phosphorylated polypeptides in a
CC sample. The present sequence is a peptide from a human phosphoprotein,
CC containing a phosphorylation site, identified by the method of the
CC invention.
XX
SQ Sequence 12 AA;
Query Match 33.0%; Score 32; DB 9; Length 12;
Best Local Similarity 85.7%; Pred. No. 3.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 11 PPTAPGT 17
:|:|:|
3 PPTAPGT 9
DB

Search completed: May 30, 2006, 15:04:08
Job time : 64.6667 secs

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OW protein - protein search, using sw model

Run on: May 30, 2006, 15:17:23 ; Search time 49.3333 Seconds
(without alignments)
169.011 Million cell updates/sec

Title: US-10-758-165A-9
Perfect score: 97
Sequence: 1 VDGOKATNIFPYTAPGTK 18

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2097797 seqs, 463214858 residues
Total number of hits satisfying chosen parameters: 432914

Minimum DB seq length: 0
Maximum DB seq length: 18

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	97	100.0	18	US-10-758-165-9	Sequence 9, Appli
2	87	89.7	18	US-10-758-165-10	Sequence 10, Appli
3	55	56.7	18	US-10-758-165-12	Sequence 12, Appli
4	37	38.1	15	US-10-856-118-34	Sequence 34, Appli
5	34	35.1	15	US-10-052-788-5	Sequence 5, Appli
6	34	35.1	18	US-10-758-165-11	Sequence 11, Appli
7	32	33.0	9	US-09-920-262A-6	Sequence 6, Appli
8	32	33.0	9	US-10-912-994-6	Sequence 6, Appli
9	32	33.0	9	US-10-975-883-6	Sequence 6, Appli
10	32	33.0	9	US-10-975-740A-6	Sequence 6, Appli
11	32	33.0	9	US-10-975-708-6	Sequence 6, Appli
12	32	33.0	9	US-10-846-019A-14	Sequence 14, Appli
13	32	33.0	11	US-10-808-187-1387	Sequence 1387, Ap
14	32	33.0	11	US-10-807-807-1387	Sequence 1387, Ap
15	32	33.0	11	US-11-004-399-2080	Sequence 2080, Ap
16	32	33.0	12	US-09-813-653-26	Sequence 26, Appli
17	32	33.0	12	US-10-862-195-1037	Sequence 1037, Ap
18	32	33.0	15	US-10-776-224-64	Sequence 64, Appli
19	32	33.0	15	US-10-530-061-1511	Sequence 1511, Ap
20	31	32.0	13	US-10-300-694A-64	Sequence 64, Appli
21	31	32.0	14	US-09-329-751A-16	Sequence 16, Appli
22	31	32.0	15	US-10-530-061-1527	Sequence 1527, Ap
23	31	32.0	18	US-10-685-898-81	Sequence 81, Appli
24	30	30.9	3	US-09-865-548A-126	Sequence 126, App
25	30	30.9	9	US-10-705-459-126	Sequence 126, App
26	30	30.9	18	US-10-195-730-360	Sequence 360, App
27	30	30.9	18	US-10-799-747-360	Sequence 360, App

28	30	30.9	18	US-10-979-183-360	Sequence 360, App
29	29	29.9	9	US-10-482-430-40	Sequence 40, Appli
30	29	29.9	9	US-11-009-840A-214	Sequence 214, App
31	29	29.9	9	US-11-009-873A-214	Sequence 214, App
32	29	29.9	9	US-11-009-769A-214	Sequence 214, App
33	29	29.9	12	US-10-894-672-39	Sequence 39, Appli
34	29	29.9	12	US-10-996-316-39	Sequence 39, Appli
35	29	29.9	12	US-11-171-567-39	Sequence 39, Appli
36	29	29.9	15	US-10-783-455-9	Sequence 9, Appli
37	29	29.9	15	US-10-720-831-20	Sequence 20, Appli
38	29	29.9	17	US-09-992-896-51	Sequence 51, Appli
39	29	29.9	17	US-10-306-631-76	Sequence 76, Appli
40	29	29.9	18	US-10-846-548A-1	Sequence 1, Appli
41	28	28.9	9	US-10-160-506-34	Sequence 34, Appli
42	28	28.9	9	US-10-449-379-34	Sequence 34, Appli
43	28	28.9	9	US-10-688-015-34	Sequence 34, Appli
44	28	28.9	9	US-10-160-505-34	Sequence 34, Appli
45	28	28.9	9	US-10-482-284A-186	Sequence 186, App

ALIGNMENTS

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RESULT 1
US-10-758-165-9
; Sequence 9, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-758-165-9

Query Match      100.0%; Score 97; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 1e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VDGOKATNIFPYTAPGTK 18
      |||||
Db      1 VDGOKATNIFPYTAPGTK 18

RESULT 2
US-10-758-165-10
; Sequence 10, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Felis catus
US-10-758-165-10

Query Match      89.7%; Score 87; DB 5; Length 18;

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Best Local Similarity 100.0%; Pred. No. 4.4e-07;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VDGOKATNIFPYTAPG 16
|||:|||||
Db 1 VDGOKATNIFPYTAPG 16

RESULT 3

US-10-758-165-12
; Sequence 12, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hamnerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Sus scrofa
US-10-758-165-12

Query Match 56.7%; Score 55; DB 5; Length 18;
Best Local Similarity 66.7%; Pred. No. 0.079;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 VDGOKATNIFPYTAP 15
|||:|||||
Db 1 VDGOKATNIFPYTAP 15

RESULT 4

US-10-856-118-34
; Sequence 34, Application US/10856118
; Publication No. US20050025747A1
; GENERAL INFORMATION:
; APPLICANT: Laidlaw, Stephen
; APPLICANT: Skinner, Mike
; APPLICANT: Hill, Adrian V.S.
; APPLICANT: Anderson, Richard
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: 3742.1000-000
; CURRENT APPLICATION NUMBER: US/10/856,118
; CURRENT FILING DATE: 2004-05-27
; PRIOR APPLICATION NUMBER: PCT/GB02/005411
; PRIOR FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: GB0128733.3
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/334,649
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Flanking sequence
US-10-856-118-34

Query Match 38.1%; Score 37; DB 5; Length 15;
Best Local Similarity 55.6%; Pred. No. 58;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 7 TNIPYPTAP 15
|||:|||||

Db 2 TNVPEYDVP 10

RESULT 5
US-10-052-788-5
; Sequence 5, Application US/10052788
; Publication No. US20030087314A1
; GENERAL INFORMATION:
; APPLICANT: Gershwin, Laurel J.
; APPLICANT: Pettigrew, Howard David
; APPLICANT: Kallina, Warren V.
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Epsilon Immunoglobulin Chain Derived Peptides for
; FILE REFERENCE: 023070-121000US
; CURRENT APPLICATION NUMBER: US/10/052,788
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: epitope peptide
; OTHER INFORMATION: P5, middle portion of C2 of equine IGE epsilon
US-10-052-788-5

Query Match 35.1%; Score 34; DB 4; Length 15;
Best Local Similarity 54.5%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 VDGOKATNIFP 11
:|||||
Db 2 IDGQKVDEQFP 12

RESULT 6

US-10-758-165-11
; Sequence 11, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hamnerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Equus caballus
US-10-758-165-11

Query Match 35.1%; Score 34; DB 5; Length 18;
Best Local Similarity 54.5%; Pred. No. 2.2e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 VDGOKATNIFP 11
:|||||
Db 1 IDGQKVDEQFP 11

RESULT 7

US-09-920-262A-6
; Sequence 6, Application US/09920262A
; Publication No. US20030124123A1
; GENERAL INFORMATION:
; APPLICANT: Shealy, David

Wed May 31 06:05:28 2006

```

; APPLICANT: Knight, David
; APPLICANT: Scallion, Bernie
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Pettit, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0248
; CURRENT APPLICATION NUMBER: US/09/920,262A
; PRIOR FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: 60/223,358
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 60/236,827
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-920-262A-6
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Query Match          33.0%; Score 32; DB 3; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.9e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY      8 NIPYPT 13
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        4 NIPYPT 9
DB
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RESULT 8
US-10-912-994-6
; Sequence 6, Application US/10912994
; Publication No. US2005002937A1
; GENERAL INFORMATION:
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Knight, David
; APPLICANT: Pettit, David
; APPLICANT: Scallion, Bernie
; APPLICANT: Shealy, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES
; FILE REFERENCE: CEN0248DIY1
; CURRENT APPLICATION NUMBER: US/10/912,994
; CURRENT FILING DATE: 2004-08-06
; PRIOR APPLICATION NUMBER: US 60/223,358
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 60/236,827
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 09/920,262
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-912-994-6
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```

Query Match          33.0%; Score 32; DB 5; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.9e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      8 NIPYPT 13
        ||:||||
        4 NIPYPT 9
DB
```

```

RESULT 9
US-10-975-883-6
; Sequence 6, Application US/10975883
; Publication No. US2005011217A1
; GENERAL INFORMATION:
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Knight, David
```

```

; APPLICANT: Pettit, David
; APPLICANT: Scallion, Bernie
; APPLICANT: Shealy, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES AND USES
; FILE REFERENCE: CEN0248DIY04
; CURRENT APPLICATION NUMBER: US/10/975,883
; CURRENT FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: US 60/223,358
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 60/236,827
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 09/920,262
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-975-883-6
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Query Match          33.0%; Score 32; DB 5; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.9e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
QY      8 NIPYPT 13
        ||:||||
        4 NIPYPT 9
DB
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RESULT 10
US-10-975-740A-6
; Sequence 6, Application US/10975740A
; Publication No. US20050196838A1
; GENERAL INFORMATION:
; APPLICANT: Giles-Komar, Jill
; APPLICANT: Knight, David
; APPLICANT: Pettit, David
; APPLICANT: Scallion, Bernie
; APPLICANT: Shealy, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES AND NUCLEIC ACIDS
; FILE REFERENCE: CEN0248DIY03
; CURRENT APPLICATION NUMBER: US/10/975,740A
; CURRENT FILING DATE: 2004-01-28
; PRIOR APPLICATION NUMBER: US 60/223,358
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 60/236,827
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 09/920,262
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-975-740A-6
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Query Match          33.0%; Score 32; DB 5; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.9e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
QY      8 NIPYPT 13
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        4 NIPYPT 9
DB
```

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RESULT 11
US-10-975-708-6
; Sequence 6, Application US/10975708
; Publication No. US20050214293A1
; GENERAL INFORMATION:
; APPLICANT: Giles-Komar, Jill
```

```

; APPLICANT: Knight, David
; APPLICANT: Peritt, David
; APPLICANT: Scallion, Bernie
; APPLICANT: Shealy, David
; TITLE OF INVENTION: ANTI-IL-12 ANTIBODIES AND COMPOSITIONS
; FILE REFERENCE: CEN0248DI02
; CURRENT APPLICATION NUMBER: US/10/975,708
; CURRENT FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: US 60/223,358
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: US 60/236,827
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US 09/920,262
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver 3.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-975-708-6
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```

Query Match          33.0%; Score 32; DB 5; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.9e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      8 NIPYPT 13
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Db      4 NIPYPT 9
```

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RESULT 12
US-10-246-019A-14
; Sequence 14, Application US/10246019A
; Publication No. US20060073133A1
; GENERAL INFORMATION:
; APPLICANT: Kikly, Kristine K.
; APPLICANT: Abrahamson, Julie
; TITLE OF INVENTION: Sialoschesin Factor-3 Antibodies
; FILE REFERENCE: GH5019-1C1
; CURRENT APPLICATION NUMBER: US/10/246,019A
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: USSN 09/577,930
; PRIOR FILING DATE: 2000-01-22
; PRIOR APPLICATION NUMBER: USSN 09/046,736
; PRIOR FILING DATE: 1998-03-24
; PRIOR APPLICATION NUMBER: USSN 60/041,885
; PRIOR FILING DATE: 1997-04-02
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human
US-10-246-019A-14
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Query Match          33.0%; Score 32; DB 5; Length 9;
Best Local Similarity 83.3%; Pred. No. 1.9e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Qy      8 NIPYPT 13
        ||:||||
Db      4 NIPYPT 9
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RESULT 13
US-10-808-187-1387
; Sequence 1387, Application US/10808187
; Publication No. US2005003009A1
; GENERAL INFORMATION:
; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
```

```

; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN
; TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE
; FILE REFERENCE: V9661.0078
; CURRENT APPLICATION NUMBER: US/10/808,187
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,031
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: 60/457,730
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/459,931
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/460,357
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/461,265
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/462,805
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/468,139
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: 60/464,886
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 60/471,200
; PRIOR FILING DATE: 2003-05-16
; NUMBER OF SEQ ID NOS: 2476
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 1387
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human severe acute respiratory system virus
US-10-808-187-1387
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Query Match          33.0%; Score 32; DB 5; Length 11;
Best Local Similarity 54.5%; Pred. No. 2.8e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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Qy      3 GOKANIPYPT 13
        ||:||||
Db      1 GOSOSNIPPT 11
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RESULT 14
US-10-807-807-1387
; Sequence 1387, Application US/10807807
; Publication No. US20050181357A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, FREDERICK C.
; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN M.
; TITLE OF INVENTION: A HIGH-THROUGHPUT DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS
; FILE REFERENCE: V9661.0077
; CURRENT APPLICATION NUMBER: US/10/807,807
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,031
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: 60/457,730
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/459,931
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/460,357
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/461,265
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/462,805
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/464,886
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; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 60/465,738
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: 60/470,935
; PRIOR FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 2487
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 1387
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Human severe acute respiratory system virus
US-10-807-807-1387

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Query Match          33.0%; Score 32; DB 5; Length 11;
Best Local Similarity 54.5%; Pred. No. 2.8e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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QY      3 GQKATNIPPYT 13
      ||:|||||
Db      1 GQSOSNIIIPQT 11

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RESULT 15
US-11-004-399-2080
; Sequence 2080, Application US/11004399
; Publication No. US20060053516A1
; GENERAL INFORMATION:
; APPLICANT: Chye, Wee Lee
; APPLICANT: Li, Hong Ye
; APPLICANT: Ramalingam, Sathiskumar
; APPLICANT: Poon, Leo Lit Man
; APPLICANT: Peiris, Joseph Sriyal Malik
; TITLE OF INVENTION: Genetically Modified Plants Comprising SARS-Cov Viral Nucleotide
; FILE REFERENCE: 2587/73166/RDK
; CURRENT APPLICATION NUMBER: US/11/004,399
; PRIOR FILING DATE: 2004-12-03
; PRIOR APPLICATION NUMBER: US 60/527,637
; PRIOR FILING DATE: 2003-12-03
; NUMBER OF SEQ ID NOS: 4043
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2080
; LENGTH: 11
; TYPE: PRT
; ORGANISM: SARS-Cov Virus
US-11-004-399-2080

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Query Match          33.0%; Score 32; DB 6; Length 11;
Best Local Similarity 54.5%; Pred. No. 2.8e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

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QY      3 GQKATNIPPYT 13
      ||:|||||
Db      1 GQSOSNIIIPQT 11

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Job time : 50.3333 secs

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GenCore version 5.1.8
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OM protein - protein search, using 6w model

Run on: May 30, 2006, 15:17:53 ; Search time 4 Seconds
(without alignments)
50.118 Million cell updates/sec

Title: US-10-758-165A-9
Perfect score: 97
Sequence: 1 VDGQKATNIPFYTAPGTX 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 1113735 residues

Total number of hits satisfying chosen parameters: 11661

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28.9	9	7	US-11-219-563-34	Sequence 34, Appl
2	26.8	9	7	US-11-254-182-12	Sequence 12, Appl
3	24.7	16	1	US-09-731-899-19	Sequence 19, Appl
4	23.7	9	6	US-10-522-356-3	Sequence 3, Appl
5	23.7	9	7	US-11-252-276-38	Sequence 83, Appl
6	23.7	9	7	US-11-023-959A-83	Sequence 83, Appl
7	23.7	10	6	US-10-538-066-747	Sequence 747, App
8	23.7	10	7	US-11-219-563-16	Sequence 16, Appl
9	23.7	12	7	US-11-106-014-82	Sequence 82, Appl
10	23.7	12	7	US-11-177-358C-16	Sequence 16, Appl
11	23.7	12	7	US-11-177-359C-16	Sequence 16, Appl
12	23.7	12	7	US-11-177-340C-16	Sequence 16, Appl
13	23.7	12	7	US-11-122-986-799	Sequence 799, Appl
14	23.7	13	7	US-11-134-228A-8	Sequence 8, Appl
15	23.7	17	7	US-11-257-498-59	Sequence 59, Appl
16	23.7	17	7	US-11-121-282-63	Sequence 63, Appl
17	23.7	17	7	US-11-251-734-30	Sequence 30, Appl
18	23.7	18	7	US-11-257-498-53	Sequence 53, Appl
19	22.7	9	7	US-11-297-317-21	Sequence 21, Appl
20	22.7	9	7	US-11-140-487A-211	Sequence 211, App
21	22.7	9	7	US-11-140-487A-348	Sequence 348, App
22	22.7	10	7	US-11-140-487A-1314	Sequence 1314, Ap
23	22.7	10	7	US-11-140-487A-1346	Sequence 1346, Ap
24	22.7	11	6	US-10-540-431-5	Sequence 5, Appl
25	22.7	12	7	US-11-122-986-656	Sequence 656, App

26	22.7	17	7	US-11-121-482-52	Sequence 52, Appl
27	21.6	9	7	US-11-055-093-222	Sequence 222, App
28	21.6	9	7	US-11-140-487A-120	Sequence 120, App
29	21.6	9	7	US-11-140-487A-551	Sequence 551, App
30	21.6	9	7	US-11-140-487A-1214	Sequence 1214, Ap
31	21.6	10	7	US-11-055-093-223	Sequence 223, App
32	21.6	10	7	US-11-140-487A-1596	Sequence 1596, Ap
33	21.6	11	6	US-10-540-431-11	Sequence 11, Appl
34	21.6	11	7	US-11-177-358C-3	Sequence 3, Appl
35	21.6	11	7	US-11-177-359C-3	Sequence 3, Appl
36	21.6	12	1	US-09-784-950-21	Sequence 21, Appl
37	21.6	12	1	US-11-177-340C-3	Sequence 7, Appl
38	20.6	9	6	US-10-538-066-7	Sequence 8, Appl
39	20.6	9	6	US-10-538-066-8	Sequence 8, Appl
40	20.6	9	7	US-11-140-487A-8	Sequence 24, Appl
41	20.6	9	7	US-11-140-487A-24	Sequence 212, App
42	20.6	9	7	US-11-140-487A-212	Sequence 327, App
43	20.6	9	7	US-11-140-487A-327	Sequence 443, App
44	20.6	9	7	US-11-140-487A-443	Sequence 472, App
45	20.6	9	7	US-11-140-487A-472	

ALIGNMENTS

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RESULT 1
US-11-219-563-34
; Sequence 34, Application US/11219563
; Publication No. US20060088539A1
; GENERAL INFORMATION:
; APPLICANT: Bandet, Neil
; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
; FILE REFERENCE: 13651.001 (BZL-001)
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US/11/219,563
; PRIOR FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: US 10/379,838
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 10/449,379
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-219-563-34

Query Match      28.9%; Score 28; DB 7; Length 9;
Best Local Similarity 63.6%; Pred. No. 5.2e+04;
Matches 7; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

QY      3 GOKATNIPFYT 13
Db      1 GOSYI--FPYT 9

RESULT 2
US-11-254-182-12
; Sequence 12, Application US/11254182
; Publication No. US20060088523A1
; GENERAL INFORMATION:
; APPLICANT: ANDYA, JAMES
; APPLICANT: GWEE, SHIANG C.
; APPLICANT: LIU, JUN
; APPLICANT: SHEN, YE
; TITLE OF INVENTION: ANTIBODY FORMULATIONS
; FILE REFERENCE: P2104R1
; CURRENT APPLICATION NUMBER: US/11/254,182
; CURRENT FILING DATE: 2005-10-19
; PRIOR APPLICATION NUMBER: US 60/620,413
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; PRIOR FILING DATE: 2004-10-20
; NUMBER OF SEQ ID NOS: 74
; SEQ ID NO 12
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-254-182-12

Query Match          26.8%; Score 26; DB 7; Length 9;
Best Local Similarity 80.0%; Pred. No. 5.2e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      9 IFPYT 13
       1:|1|1|
       5 IYPYT 9

Db

RESULT 3
US-09-731-899-19
; Sequence 19, Application US/09731899
; Publication No. US20060088548A1
; GENERAL INFORMATION:
; APPLICANT: Chai, Benjamin
; TITLE OF INVENTION: CHIMERIC PEPTIDES AS IMMUNOGENS, ANTIBODIES THEREOF, AND METHODS
; FILE REFERENCE: 2055/1203433-US1
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/169,687
; PRIOR FILING DATE: 1999-12-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Tetanus toxin bacteria
US-09-731-899-19

Query Match          24.7%; Score 24; DB 1; Length 16;
Best Local Similarity 44.4%; Pred. No. 2.1e+02;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      7 TNIFPYTAP 15
       1:|1|1|
       3 STVPIYIGP 11

Db

RESULT 4
US-10-522-356-3
; Sequence 3, Application US/10522356
; Publication No. US20060105323A1
; GENERAL INFORMATION:
; APPLICANT: WHITEHEAD, CHRISTOPHER BRUCE ALEXANDER
; APPLICANT: CLARK, ANTHONY JOHN
; APPLICANT: MOLE, CHARLES ROLAND
; TITLE OF INVENTION: MULTI-REPORTER GENE MODEL FOR TOXICOLOGICAL SCREENING
; FILE REFERENCE: 102286.155 US1
; CURRENT FILING DATE: 2005-01-26
; PRIOR APPLICATION NUMBER: PCT/GB03/003192
; PRIOR FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: GB 0217402.7
; PRIOR FILING DATE: 2002-07-26
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Sequence: Haemagglutinin
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```

; OTHER INFORMATION: epitope from unknown organism
US-10-522-356-3

Query Match          23.7%; Score 23; DB 6; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.2e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      10 FPYTAP 15
       1:|1|1|
       1 YPYDVP 6

Db

RESULT 5
US-11-252-276-38
; Sequence 38, Application US/11252276
; Publication No. US20060094868A1
; GENERAL INFORMATION:
; APPLICANT: Giuliano, Kenneth A.
; APPLICANT: Bright, Gary
; APPLICANT: Olson, Keith
; APPLICANT: Burroughs-Tencza, Sarah
; TITLE OF INVENTION: A System for Cell Based Screening
; FILE REFERENCE: 97-022-K2-CO
; CURRENT FILING DATE: 2005-10-17
; PRIOR APPLICATION NUMBER: 09/713,572
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: 09/430,656
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 09/398,965
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 09/031,271
; PRIOR FILING DATE: 1998-02-27
; PRIOR APPLICATION NUMBER: 08/810,983
; PRIOR FILING DATE: 1997-02-27
; PRIOR APPLICATION NUMBER: 60/136,078
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 60/106,308
; PRIOR FILING DATE: 1998-10-30
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 38
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HA epitope
US-11-252-276-38

Query Match          23.7%; Score 23; DB 7; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.2e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      10 FPYTAP 15
       1:|1|1|
       1 YPYDVP 6

Db

RESULT 6
US-11-023-959A-83
; Sequence 83, Application US/11023959A
; Publication No. US20060106203A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; TITLE OF INVENTION: Ligand
; FILE REFERENCE: 8039/2142
; CURRENT FILING DATE: 2004-12-28
; PRIOR APPLICATION NUMBER: PCT/GB03/002804
; PRIOR FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 187
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 83
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; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: HA tag
US-11-023-959A-83

Query Match      23.7%; Score 23; DB 7; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.2e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      10 PPYAP 15
Db      1 YPYDVP 6

RESULT 7
US-10-538-066-747
; Sequence 747, Application US/10538066
; Publication No. US20060094649A1
; GENERAL INFORMATION:
; APPLICANT: Edimmune Inc.
; TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen
; TITLE OF INVENTION: Peptides and Compositions
; FILE REFERENCE: 2060.015PC06
; CURRENT APPLICATION NUMBER: US/10/538,066
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US 60/432,017
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 767
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 747
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: A3 non-natural consensus peptide
US-10-538-066-747

Query Match      23.7%; Score 23; DB 6; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.9e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      9 IFPY 12
Db      2 VFY 5

RESULT 8
US-11-219-563-16
; Sequence 16, Application US/11219563
; Publication No. US20060088539A1
; GENERAL INFORMATION:
; APPLICANT: Bander, Neil
; TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
; TITLE OF INVENTION: MEMBRANE ANTIGEN AND USES THEREOF
; FILE REFERENCE: 13651.001 (BZL-001)
; CURRENT APPLICATION NUMBER: US/11/219,563
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: PCT/US04/06586
; PRIOR FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: US 10/379,838
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 10/449,379
; PRIOR FILING DATE: 2003-05-30
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: deimmunized light chain J591
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US-11-219-563-16

Query Match      23.7%; Score 23; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      15 PGTK 18
Db      3 PGTK 6

RESULT 9
US-11-106-014-82
; Sequence 82, Application US/11106014
; Publication No. US2006008846A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, Michele
; APPLICANT: Chiau, Dah Shaim
; APPLICANT: Latres, Esther
; APPLICANT: Sivasava, Promod
; APPLICANT: Chandawarkar, Rajiv
; TITLE OF INVENTION: OF PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT
; FILE REFERENCE: 5914-106-999
; CURRENT APPLICATION NUMBER: US/11/106,014
; CURRENT FILING DATE: 2005-04-13
; PRIOR APPLICATION NUMBER: 10/632,150
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 09/385,219
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1997-03-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-106-014-82

Query Match      23.7%; Score 23; DB 7; Length 12;
Best Local Similarity 46.2%; Pred. No. 2.3e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY      2 DQKATNIPYTA 14
Db      2 DGEKDT--YSYLA 12

RESULT 10
US-11-177-358C-16
; Sequence 16, Application US/11177358C
; Publication No. US20060094072A1
; GENERAL INFORMATION:
; APPLICANT: CAMPBELL, DOUGLAS A.
; TITLE OF INVENTION: PEPTIDE SEQUENCE TAGS AND METHOD OF USING SAME
; FILE REFERENCE: 113703-1006
; CURRENT APPLICATION NUMBER: US/11/177,358C
; CURRENT FILING DATE: 2005-07-11
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
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US-11-177-358C-16

Query Match 23.7%; Score 23; DB 7; Length 12;
Best Local Similarity 57.1%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 PPYTAPG 16
DB 1 FPCDGP 7

RESULT 11

US-11-177-359C-16
; Sequence 16, Application US/11177359C
; Publication No. US20060094058A1
; GENERAL INFORMATION:
; APPLICANT: CAMPBELL, DOUGLAS A.
; TITLE OF INVENTION: PEPTIDE SEQUENCE TAGS AND METHOD OF USING SAME
; FILE REFERENCE: 113703-1004
; CURRENT APPLICATION NUMBER: US/11/177,359C
; CURRENT FILING DATE: 2005-07-11
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 12
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
US-11-177-359C-16

Query Match 23.7%; Score 23; DB 7; Length 12;
Best Local Similarity 57.1%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 PPYTAPG 16
DB 1 FPCDGP 7

RESULT 12
US-11-177-340C-16
; Sequence 16, Application US/11177340C
; Publication No. US2006009663A1
; GENERAL INFORMATION:
; APPLICANT: CAMPBELL, DOUGLAS A.
; TITLE OF INVENTION: PEPTIDE SEQUENCE TAGS AND METHOD OF USING SAME
; FILE REFERENCE: 113703-1005
; CURRENT APPLICATION NUMBER: US/11/177,340C
; CURRENT FILING DATE: 2005-07-11
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 12
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide
US-11-177-340C-16

Query Match 23.7%; Score 23; DB 7; Length 12;
Best Local Similarity 57.1%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 PPYTAPG 16
DB 1 FPCDGP 7

RESULT 13
US-11-122-986-799
; Sequence 799, Application US/11122986
; Publication No. US20060104989A1

; GENERAL INFORMATION:
; APPLICANT: EDWARDS, ALED
; APPLICANT: DHARAMSI, AKIL
; APPLICANT: VEDADI, MASOUD
; TITLE OF INVENTION: ESSENTIAL NOVEL BACTERIAL POLYPEPTIDES
; FILE REFERENCE: IPT-330.01
; CURRENT APPLICATION NUMBER: US/11/122,986
; CURRENT FILING DATE: 2005-05-05
; PRIOR APPLICATION NUMBER: 60/423,875
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,832
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,915
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,757
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,758
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/424,367
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,376
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,370
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,362
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,373
; PRIOR FILING DATE: 2002-11-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 844
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 799
; LENGTH: 12
; TYPE: PRP
; ORGANISM: Streptococcus pneumoniae
US-11-122-986-799

Query Match 23.7%; Score 23; DB 7; Length 12;
Best Local Similarity 61.5%; Pred. No. 8.3e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 2; Gaps 2;

QY 7 TNIPYT-APGTX 18
DB 1 SNI-PYTWGTX 12

RESULT 14
US-11-134-228A-8
; Sequence 8, Application US/11134228A
; Publication No. US20060105320A1
; GENERAL INFORMATION:
; APPLICANT: Lindquist et al.
; TITLE OF INVENTION: ELECTRICAL CONDUCTORS AND DEVICES FROM PRION-LIKE PROTEINS
; FILE REFERENCE: 30554/40155A
; CURRENT APPLICATION NUMBER: US/11/134,228A
; CURRENT FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 60/573,277
; PRIOR FILING DATE: 2004-05-20
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 13
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Hemagglutinin
US-11-134-228A-8

Query Match 23.7%; Score 23; DB 7; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Wed May 31 06:05:28 2006

QY 10 PPYTAP 15
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Db 1 YPYDVP 6

RESULT 15

US-11-257-498-59
; Sequence 59, Application US/11257498
; Publication No. US20060088550A1
; GENERAL INFORMATION:
; APPLICANT: Bachmann, Martin F
; APPLICANT: Pulurija, Alma
; APPLICANT: Saudan, Philippe
; TITLE OF INVENTION: Gastric Inhibitory Polypeptide (GIP) Antigen Arrays and Used therefor
; FILE REFERENCE: 1700.0540001
; CURRENT APPLICATION NUMBER: US/11/257,498
; PRIOR FILING DATE: 2005-10-25
; PRIOR APPLICATION NUMBER: 60/621,465
; PRIOR FILING DATE: 2004-10-25
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 59
; LENGTH: 17
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: CGGPKPSTPPGSSGGAP
US-11-257-498-59

Query Match 23.7%; Score 23; DB 7; Length 17;
Best Local Similarity 57.1%; Pred. No. 3.3e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 11 PPYTAP 17
:||||
Db 6 PSTPPGS 12

Search completed: May 30, 2006, 15:20:31
Job time : 4 secs

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Wed May 31 06:05:24 2006

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OM protein - protein search, using sw model

Run on: May 30, 2006, 09:59:16 ; Search time 20.3333 Seconds
(without alignments)
64.572 Million cell updates/sec

Title: US-10-758-165A-3
Perfect score: 74
Sequence: 1 RNNVLIQTDQQTTR 15

Scoring table:
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Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 249102

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Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	37.8	10	3	US-09-641-528B-4809
2	28	37.8	11	3	US-09-641-528B-4810
3	28	37.8	11	3	US-09-641-528B-4856
4	28	37.8	11	3	US-09-641-528B-13626
5	28	37.8	11	3	US-09-641-528B-26703
6	28	37.8	15	3	US-09-641-528B-47147
7	28	37.8	15	3	US-09-641-528B-50653
8	26	35.1	9	3	US-09-641-528B-4922
9	26	35.1	9	3	US-09-641-528B-50984
10	26	35.1	10	3	US-09-641-528B-4923
11	26	35.1	10	3	US-09-641-528B-26799
12	25	33.8	14	2	US-09-378B-7
13	25	33.8	15	5	PCR-US95-04018-42
14	25	33.8	11	1	US-08-456-670B-38
15	24	32.4	11	2	US-09-372-036-38
16	24	32.4	13	2	US-10-112-582A-14
17	24	32.4	15	1	US-08-403-378B-7
18	24	32.4	15	3	US-09-641-528B-46828
19	24	32.4	8	3	US-09-641-528B-4862
20	23	31.1	9	3	US-09-641-528B-4808
21	23	31.1	9	3	US-09-641-528B-4863
22	23	31.1	9	3	US-09-641-528B-4863
23	23	31.1	9	3	US-09-641-528B-13652
24	23	31.1	9	3	US-09-641-528B-26750
25	23	31.1	10	2	US-08-485-324-4
26	23	31.1	10	2	US-08-485-324-30

27	23	31.1	10	2	US-08-447-906-4	Sequence 4, Appl
28	23	31.1	10	2	US-08-447-506-10	Sequence 30, Appl
29	23	31.1	10	2	US-08-235-437-4	Sequence 4, Appl
30	23	31.1	10	2	US-08-235-437-30	Sequence 30, Appl
31	23	31.1	10	2	US-08-447-515-4	Sequence 4, Appl
32	23	31.1	10	2	US-08-447-515-30	Sequence 4, Appl
33	23	31.1	10	2	US-09-462-645C-29	Sequence 29, Appl
34	23	31.1	10	2	US-09-573-830-4	Sequence 4, Appl
35	23	31.1	10	2	US-09-573-830-30	Sequence 30, Appl
36	23	31.1	10	3	US-09-641-528B-4855	Sequence 4855, Ap
37	23	31.1	11	3	US-09-641-528B-4860	Sequence 4860, Ap
38	23	31.1	12	2	US-08-479-233-8	Sequence 8, Appl
39	23	31.1	12	2	US-09-392-812A-7	Sequence 7, Appl
40	23	31.1	12	5	PCT-US93-00643-8	Sequence 8, Appl
41	23	31.1	14	2	US-10-394-980-55	Sequence 55, Appl
42	23	31.1	15	2	US-09-700-993-6	Sequence 6, Appl
43	22	29.7	5	1	US-08-762-106-19	Sequence 19, Appl
44	22	29.7	5	2	US-09-320-774-19	Sequence 19, Appl
45	22	29.7	6	1	US-08-762-106-17	Sequence 17, Appl

ALIGNMENTS

```
RESULT 1
US-09-641-528B-4809
; Sequence 4809, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Estebean
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIORITY FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4809
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-4809
;
Query Match          37.8%; Score 28; DB 3; Length 10;
Best Local Similarity 40.0%; Pred. No. 70;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY      5 LIQDQQT 14
Db      1 MVQVEEQQT 10
RESULT 2
US-09-641-528B-4810
; Sequence 4810, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Estebean
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
```

```

; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 4810
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-4810

Query Match          37.8%; Score 28; DB 3; Length 11;
Best Local Similarity 40.0%; Pred. No. 78;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 5 LIOTDQOATT 14
DB 1 MVOVEEQOTT 10

RESULT 3
US-09-641-528B-4856
; Sequence 4856, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 4856
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-4856

Query Match          37.8%; Score 28; DB 3; Length 11;
Best Local Similarity 40.0%; Pred. No. 78;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 5 LIOTDQOATT 14
DB 2 MVOVEEQOTT 11

RESULT 4
US-09-641-528B-13626
; Sequence 13626, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard

; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 13626
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-13626

Query Match          37.8%; Score 28; DB 3; Length 11;
Best Local Similarity 40.0%; Pred. No. 78;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 5 LIOTDQOATT 14
DB 1 MVOVEEQOTT 10

RESULT 5
US-09-641-528B-26703
; Sequence 26703, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 26703
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-26703

Query Match          37.8%; Score 28; DB 3; Length 11;
Best Local Similarity 40.0%; Pred. No. 78;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 5 LIOTDQOATT 14
DB 1 MVOVEEQOTT 10

RESULT 6
US-09-641-528B-47147
; Sequence 47147, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
```

```

; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47147
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-47147

Query Match      37.8%; Score 28; DB 3; Length 15;
Best Local Similarity 40.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      5 LIOTDOQATT 14
        ::::|
Db      1 MVEVEQOTT 10

RESULT 7
US-09-641-528B-50653
; Sequence 50653, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50653
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-50653

Query Match      37.8%; Score 28; DB 3; Length 15;
Best Local Similarity 40.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      5 LIOTDOQATT 14
        ::::|
Db      3 MVEVEQOTT 12

RESULT 8
US-09-641-528B-4922
; Sequence 4922, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert

; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4922
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-4922

Query Match      35.1%; Score 26; DB 3; Length 9;
Best Local Similarity 44.4%; Pred. No. 5e+05;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      6 IOTDOQATT 14
        ::::|
Db      1 VVEVEQOTT 9

RESULT 9
US-09-641-528B-50984
; Sequence 50984, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 50984
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-50984

Query Match      35.1%; Score 26; DB 3; Length 9;
Best Local Similarity 44.4%; Pred. No. 5e+05;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      6 IOTDOQATT 14
        ::::|
Db      1 VVEVEQOTT 9

RESULT 10
US-09-641-528B-4923
; Sequence 4923, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
```

```

; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Eteban
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT FILING DATE: 1999-01-25
; CURRENT APPLICATION NUMBER: US/09/641,528B
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4923
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-4923
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Query Match          35.1%; Score 26; DB 3; Length 10;
Best Local Similarity 44.4%; Pred. No. 1.6e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      6 IOTDOQATT 14
       :|::|||
Db      1 VQVEQOTT 9
```

```

RESULT 11
US-09-641-528B-26799
; Sequence 26799, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Eteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26799
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-26799
```

```

Query Match          35.1%; Score 26; DB 3; Length 10;
Best Local Similarity 44.4%; Pred. No. 1.6e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      6 IOTDOQATT 14
       :|::|||
Db      1 VQVEQOTT 9
```

```

RESULT 12
US-09-236-415-6
; Sequence 6, Application US/09236415
; Patent No. 6309863
; GENERAL INFORMATION:
; APPLICANT: Anderson, Carl W.
; APPLICANT: Appella, Ettore
```

```

; APPLICANT: Sakaguchi, Kazuya
; TITLE OF INVENTION: METHODS FOR GENERATING PHOSPHORYLATION SITE-SPECIFIC
; FILE REFERENCE: U.S. Application 09/236,415
; CURRENT APPLICATION NUMBER: US/09/236,415
; CURRENT FILING DATE: 1999-01-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 6
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: POLYPEPTIDE
; OTHER INFORMATION: ANTIGEN
; FEATURE:
; OTHER INFORMATION: Residue Xaa is a phosphoserine mimetic
US-09-236-415-6
```

```

Query Match          33.8%; Score 25; DB 2; Length 14;
Best Local Similarity 54.5%; Pred. No. 3.6e+02;
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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Qy      2 NNVLIOQTDOQA 12
       :|::|||
Db      3 NNVLXPLPSQA 13
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```

RESULT 13
US-08-221-583-42
; Sequence 42, Application US/08221583
; Patent No. 5486595
; GENERAL INFORMATION:
; APPLICANT: Heavenr, George A.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Woodcock Washburn Kurtz Mackiewicz & No. 5486595r:is
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25.mdcctmod.
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,583
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: CCOR-0185
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-221-583-42
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```

Query Match          33.8%; Score 25; DB 1; Length 15;
Best Local Similarity 55.6%; Pred. No. 3.9e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      7 QTDQQATT 15
       :|::|||
```

Db 4 QVETOATR 12

RESULT 14

PCT-US95-04018-42
Sequence 42, Application PC/TUS9504018

GENERAL INFORMATION:

APPLICANT: Heavener, George A.
APPLICANT: Kruszyński, Marian
APPLICANT: Mervic, Miljenko
APPLICANT: Weber, Robert W.
TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
STREET: Norria
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19403

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04018

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-APR-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-APR-1994

ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark

REGISTRATION NUMBER: 33,229

REFERENCE/DOCKET NUMBER: CCOR-0232

TELEPHONE: (215) 568-3100

TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 42:

SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid

MOLECULE TYPE: linear

TOPOLOGY: linear

PCT-US95-04018-42

Query Match 33.8%; Score 25; DB 5; Length 15;

Best Local Similarity 55.6%; Pred. No. 3.9e+02;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Db 7 QVETOATR 15

4 QVETOATR 12

RESULT 15

US-08-456-670B-38

Sequence 38, Application US/08456670B

Patent No. 5932415

GENERAL INFORMATION:

APPLICANT: SCHUBERT, PETER

APPLICANT: NEUMANN, SIEGFRIED

APPLICANT: PAMELZIK, MARTINA

APPLICANT: LINXWEILER, WINFRIED

APPLICANT: BURGER, CHRISTA

APPLICANT: HOFMANN, GOTTFRIED

APPLICANT: ROBERT, ANDREAS

APPLICANT: GOEBEL, WERNER

APPLICANT: KOHLER, STEFAN

TITLE OF INVENTION: PROCESSES AND AGENTS FOR DETECTING

TITLE OF INVENTION: LISTERIAS

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: MULLEN, WHITE, ZELANO & BRANIGAN, P.C.

STREET: 2200 CLARENDON BLVD., SUITE 1400

CITY: ARLINGTON

STATE: VIRGINIA

COUNTRY: US

ZIP: 22201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/456,670B

FILING DATE: 01-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/412,227

FILING DATE: 27-MAR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/075,248

FILING DATE: 11-JUN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE 4239567.4

FILING DATE: 25-NOV-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE 421911.4

FILING DATE: 11-JUN-1992

ATTORNEY/AGENT INFORMATION:

NAME: HAMLET-KING, DIANA

REGISTRATION NUMBER: 33,302

REFERENCE/DOCKET NUMBER: MERCK 1694D1

TELEPHONE: 703-243-6333

TELEFAX: 703-243-6410

INFORMATION FOR SEQ ID NO: 38:

SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids

TYPE: amino acid

MOLECULE TYPE: linear

ORIGINAL SOURCE:

ORGANISM: Listeria innocua

US-08-456-670B-38

Query Match 32.4%; Score 24; DB 1; Length 11;

Best Local Similarity 57.1%; Pred. No. 4.2e+02;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 9 DQOATR 15

1 EQOTTK 7

Search completed: May 30, 2006, 11:11:06

Job time : 20.3333 secs

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 30, 2006, 09:58:55 ; Search time 11.6667 Seconds
(without alignments)
123.707 Million cell updates/sec

Title: US-10-758-165A-3
Perfect score: 74
Sequence: 1 RNNVLQTDQQTTR 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*

1: pirl:.*
2: pirl:.*
3: pirl:.*
4: pirl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	33.8	15	2	S32677
2	21	28.4	13	2	B61458
3	21	28.4	13	2	B61458
4	21	28.4	15	2	PH1329
5	20	27.0	10	2	S43625
6	19	25.7	10	2	A53695
7	19	25.7	13	2	H56046
8	19	25.7	14	2	C44823
9	18	24.3	9	2	S6636
10	18	24.3	11	2	S43626
11	18	24.3	13	2	A58491
12	18	24.3	15	2	PT0205
13	18	24.3	15	2	S72432
14	17	23.0	10	2	A61354
15	17	23.0	10	2	PH0933
16	17	23.0	11	2	G42762
17	17	23.0	11	4	S52252
18	17	23.0	12	2	A40763
19	17	23.0	13	2	S36887
20	17	23.0	13	2	E42762
21	17	23.0	13	2	PCI008
22	17	23.0	13	2	I49637
23	17	23.0	14	2	PH1705
24	17	23.0	14	2	PH0753
25	17	23.0	14	2	D35141
26	17	23.0	15	2	PA0058
27	17	23.0	15	2	D56385
28	17	23.0	15	2	S62641
29	17	23.0	15	2	B46047

30	16	21.6	10	2	D54823	olfactory receptor
31	16	21.6	10	2	C54823	olfactory receptor
32	16	21.6	11	2	S70720	trigger factor hom
33	16	21.6	12	2	A33099	163K exoantigen -
34	16	21.6	13	2	S28425	20K protein - rape
35	16	21.6	14	2	E81280	probable proteolys
36	16	21.6	15	2	PO0681	photosystem I 19.0
37	16	21.6	15	2	PS0452	32K protein 306 -
38	16	21.6	15	2	PH1631	Ig H chain V-D-J r
39	16	21.6	15	2	A45096	thyrotropin-releas
40	16	21.6	15	2	A36527	juvenile-hormone e
41	16	21.6	15	2	A53594	calnexin - mouse (
42	15	20.3	8	2	S71919	alcohol dehydrogen
43	15	20.3	8	2	T48890	hypothetical prote
44	15	20.3	10	2	P00788	NADH2 dehydrogenas
45	15	20.3	11	2	P00682	photosystem I 17.5

ALIGNMENTS

RESULT 1
S32677
nitrogenase cofactor synthesis protein nifs - Anabaena variabilis (fragment)
N:Contains: L-cysteine sulfotransferase (EC 2.8.1.-)
C:Species: Anabaena variabilis
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S32677
R:Monerjahn, U.; Boehme, H.
Submitted to the EMBL Data Library, December 1992
A:Description: Cloning and expression in E. coli of the Anabaena.
A:Reference number: S32675
A:Accession: S32677
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-15 <MON>
A:Cross-references: UNIPROT:Q04507; UNIPARC:UPI00001301C; EMBL:X69898; NID:G296503; PID
C:Superfamily: nitrogen fixation protein nifs
C:Keywords: sulfotransferase

Query Match 33.8% Score 25; DB 2; Length 15;
Best Local Similarity 45.5% Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 LIQTDQQTTR 15
DB 3 VIYLDNNATTK 13

RESULT 2
B61458
Ig kappa chain V-I region (BLA) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 16-Aug-1996
R:Bioner, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Minaesco, E.
J. Exp. Med. 170, 1551-1558, 1989
A:Title: Expression of a public idiotype by human monoclonal IGM directed to myelin-asso
A:Reference number: A61458; MUID:90039128; PMID:2478651
A:Accession: B61458
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <BRO>
A:Cross-references: UNIPARC:UPI000017C25D
C:Keywords: heterotrimer; immunoglobulin

Query Match 28.4% Score 21; DB 2; Length 13;
Best Local Similarity 55.6% Pred. No. 1e+03;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 IQTDQQTTR 14
DB 2 IQMTSPPTT 10

RESULT 3
A61458
Ig kappa chain V-I region (BCU) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 16-Aug-1996
C/Accession: A61458; PL0156
R/Brouet, J.C.; Dellagi, K.; Gerdron, M.C.; Chevaller, A.; Schmitt, C.; Minaesco, E.
J. Exp. Med. 170, 1551-1558, 1994
A/Title: Expression of a public idioType by human monoclonal IGM directed to myelin-assc
A/Reference number: A61458; MUID:90039128; PMID:2478651
A/Accession: A61458
A/Molecule type: protein
A/Residues: 1-13 <BRO>
A/Cross-references: UNIPARC:UPI000017C25E
A/Comment: This protein is one of monoclonal IGM reactive with myeloma-associated glycop
C/Keywords: heterotetramer; immunoglobulin

Query Match 28.4%; Score 21; DB 2; Length 13;
Best Local Similarity 55.6%; Pred. No. 1e+03;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 IQTDOQATT 14
|||
Db 2 IQMTQSPPT 10

RESULT 4
PH1329
Ig heavy chain DJ region (clone C552-104) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C/Accession: PH1329
R/Maserman, R.; Galli, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A/Reference number: PH1302; MUID:93094761; PMID:1460419
A/Accession: PH1329
A/Molecule type: DNA
A/Residues: 1-15 <WAS>
A/Cross-references: UNIPARC:UPI000017C245
C/Keywords: heterotetramer; immunoglobulin

Query Match 28.4%; Score 21; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 RNNVLI 6
|||
Db 4 RNEVMI 9

RESULT 5
S43625
cytochrome-c oxidase (EC 1.9.3.1) chain Va, hepatic - rainbow trout (fragment)
C/Species: Oncorhynchus mykiss (rainbow trout)
C/Date: 20-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C/Accession: S43625
R/Freund, R.; Kadenbach, B.
Eur. J. Biochem. 221, 1111-1116, 1994
A/Title: Identification of tissue-specific isoforms for subunits Vb and V1a of cytochr
A/Reference number: S43624; MUID:94237150; PMID:8181469
A/Accession: S43625
A/Molecule type: protein
A/Residues: 1-10 <FRE>
A/Cross-references: UNIPROT:P80328; UNIPARC:UPI0000128131
A/Note: the source is designated as Salmo gairdneri
C/Genetics:
A/Genome: nuclear
C/Keywords: liver; membrane-associated complex; mitochondrion; oxidoreductase

Query Match 27.0%; Score 20; DB 2; Length 10;

Best Local Similarity 33.3%; Pred. No. 1.2e+03;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 6 IQTDOQ 11
:::
Db 5 VETDDE 10

RESULT 6
A55695
proteoglycan core protein - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 17-Mar-1999
C/Accession: A55695
R/Lark, M.W.; Gordy, J.T.; Weidner, J.R.; Ayala, J.; Kimura, J.H.; Williams, H.R.; Mumfo
J. Biol. Chem. 270, 2550-2556, 1995
A/Title: Cell-mediated catabolism of aggrecan. Evidence that cleavage at the "aggrecanae
A/Reference number: A55695; MUID:95155314; PMID:7852317
A/Accession: A55695
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-10 <LAR>
A/Cross-references: UNIPARC:UPI000017C9A9

Query Match 25.7%; Score 19; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 RNNVLI 6
|||
Db 2 RGNVIL 7

RESULT 7
H56046
urinary tract stone matrix protein 10, 42K - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 09-Jul-2004
C/Accession: H56046
R/Binette, J.P.; Binette, M.B.; Gawinowicz, M.A.; Kendrick, N.
submitted to the Protein Sequence Database, February 1995
A/Description: Isolation, characterization and sequence of stone proteins.
A/Reference number: A56046
A/Accession: H56046
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-13 <BIN>
A/Cross-references: UNIPROT:Q7M4P7; UNIPARC:UPI000017C406

Query Match 25.7%; Score 19; DB 2; Length 13;
Best Local Similarity 37.5%; Pred. No. 2.5e+03;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NNVLITQTD 9
:::
Db 6 NDLAARFD 13

RESULT 8
C44823
synaptoosomal-associated protein SNAP-25 peptide 8 - rabbit (fragment)
N/Alternate names: superprotein peptide 8
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 15-Jun-1996
C/Accession: C44823
R/Lowey, A.; Liu, W.S.; Baitinger, C.; Willard, M.B.
J. Neurosci. 11, 3412-3421, 1991
A/Title: The major 35S-methionine-labeled rapidly transported protein (superprotein) is
A/Reference number: A44823; MUID:92044785; PMID:1941090
A/Accession: C44823
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-14 <LOB>

A;Cross-references: UNIPARC:UPI000017C5E7
 A;Experimental source: visual tissue
 A;Note: sequence extracted from NCBI backbone (NCBIP:64253)
 C;Keywords: membrane trafficking

Query Match 25.7%; Score 19; DB 2; Length 14;
 Best Local Similarity 42.9%; Pred. No. 2.7e+03;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 5 NVLIQDQ 11
 |||
 Db 2 LVMLDEQ 8

RESULT 9

S66636
 alpha-2-macroglobulin isoform 2 - bovine (fragment)
 C;Species: Bos primigenius indicus (zebu cattle)
 C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
 C;Accession: S66636

R;DOImer: K.; Jenner, L.B.; Jacobsen, L.; Andersen, G.R.; Koch, T.J.; Thirup, S.; Sottrup
 FEBS Lett. 372, 93-95, 1995

A;Title: Crystallization and preliminary X-ray analysis of the receptor-binding domain of
 A;Reference number: S66634; MUID:96032553; PMID:7556651

A;Accession: S66636
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-9 <DOL>
 A;Cross-references: UNIPROT:Q7M2N7; UNIPARC:UPI000017C480

Query Match 24.3%; Score 18; DB 2; Length 9;
 Best Local Similarity 37.5%; Pred. No. 2.8e+05;
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 NVLIQDQ 10
 |||
 Db 2 NILPKDE 9

RESULT 10

S43626
 cytochrome-c oxidase (EC 1.9.3.1) chain Vb-H - trout (fragment)
 C;Species: Salmo sp. (trout)
 C;Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 02-Jul-1998
 C;Accession: S43626

R;Freund, R.; Kadenbach, B.
 Eur. J. Biochem. 221, 1111-1116, 1994

A;Title: Identification of tissue-specific isoforms for subunits Vb and VIIa of cytochrome
 A;Reference number: S43624; MUID:94237150; PMID:8181469

A;Accession: S43626
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-11 <PRE>
 A;Cross-references: UNIPARC:UPI000017BF62
 C;Keywords: electron transfer; membrane-associated complex; oxidoreductase; respiratory

Query Match 24.3%; Score 18; DB 2; Length 11;
 Best Local Similarity 50.0%; Pred. No. 3.2e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 IQTDQ 11
 |||
 Db 6 IPTDE 11

RESULT 11

A59491
 epithelial dog allergen - Canis familiaris (fragment)
 C;Species: Canis familiaris
 C;Date: 27-Oct-2003 #sequence_revision 27-Oct-2003 #text_change 27-Oct-2003
 C;Accession: A59491

R;Saarelainen, S.; Taivalinen, A.; Rytku-vnen-Missinen, M.; Auriola, S.; Immonen, A.; MM-
 submitted to the Protein Sequence Database, October 2003

A;Description: Diagnosis of dog allergy with recombinant allergens.

A;Reference number: A59491
 A;Accession: A59491
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-13 <VIR>
 A;Note: IGE-binding protein; allergen

Query Match 24.3%; Score 18; DB 2; Length 13;
 Best Local Similarity 80.0%; Pred. No. 3.8e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 NVLIQ 7
 |||
 Db 3 NVLTQ 7

RESULT 12

PT0205
 insulin-like growth factor-binding protein, bone - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 08-Dec-1994
 C;Accession: PT0205; A33175

R;Bautista, C.M.; Baylink, D.J.; Mohan, S.
 Biochem. Biophys. Res. Commun. 176, 756-763, 1991

A;Title: Isolation of a novel insulin-like growth factor (IGF) binding protein from huma
 A;Reference number: PT0205; MUID:9122244; PMID:1709017
 A;Accession: PT0205
 A;Molecule type: protein
 A;Residues: 1-15 <BAU>
 A;Cross-references: UNIPARC:UPI000017C275

Query Match 24.3%; Score 18; DB 2; Length 15;
 Best Local Similarity 33.3%; Pred. No. 4.5e+03;
 Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 4 VLIQDQA 12
 |||
 Db 5 VAVPPDQA 13

RESULT 13

S72432
 epoxypropan isomerase component B - Xanthobacter sp. (strain Py2) (fragment)
 C;Species: Xanthobacter sp.
 A;Variety: strain Py2
 C;Date: 14-Apr-1998 #sequence_revision 08-May-1998 #text_change 07-May-1999
 C;Accession: S72432

R;Chan Kwo Chion, C.K.N.; Leak, D.J.
 Biochem. J. 319, 489-506, 1996

A;Title: Purification and characterization of two components of epoxypropane isomerase/c
 A;Reference number: S72431; MUID:97069704; PMID:8912687
 A;Accession: S72432
 A;Molecule type: protein
 A;Residues: 1-15 <CHA>

A;Cross-references: UNIPARC:UPI000017CA9F
 A;Note: 3-Met and 13-Peu were also found
 C;Complex: homodimer
 C;Function:
 A;Description: NADP-dependent lipamide reductase
 A;Pathway: epoxypropane degradation
 A;Note: sensitive to N-ethyl-maleimide and p-chloromercuribenzoate
 C;Keywords: FAD

Query Match 24.3%; Score 18; DB 2; Length 15;
 Best Local Similarity 44.4%; Pred. No. 4.5e+03;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 RNVLIQTD 9
 |||
 Db 7 RNDHLIXD 15

RESULT 14

A61354
carnitine medium/long chain acyltransferase (EC 2.3.1.-) - rat (fragment)
N/Alternate names: endoplasmic reticulum protein Erp61; glucose regulated protein GRP58;
C/Species: Rattus norvegicus (Norway rat)
C/Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-May-1999
C/Accession: A61354
R/Murthy, M.S.R.; Pande, S.V.
Mol. Cell. Biochem. 122, 133-138, 1993
A/Title: Carnitine medium/long chain acyltransferase of microsomes seems to be the previ
A/Reference number: A61354; MUID:94049728; PMID:8232244
A/Accession: A61354
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-10 <MUR>
A/Cross-references: UNIPARC:UPI000017C9DE
C/Keywords: acyltransferase

Query Match 23.0%; Score 17; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 4.4e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 NVLIQTQD 10
: || ||:
Db 2 DVLEETDE 9

RESULT 15

PH0933
T-cell receptor beta chain V-D-J region (clone 4) - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C/Accession: PH0933
R/Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenberg, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A/Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy
A/Reference number: PH0931; MUID:92078857; PMID:1836012
A/Accession: PH0933
A/Molecule type: mRNA
A/Residues: 1-10 <GOL>
A/Cross-references: UNIPARC:UPI000017C9E5
A/Experimental source: complete Freund's adjuvant-immunized lymph node
A/Note: the authors translated the codon CAG for residue 9 as Glu
C/Keywords: T-cell receptor

Query Match 23.0%; Score 17; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RNN 3
: || |
Db 6 RNN 8

Search completed: May 30, 2006, 10:13:21
Job time : 13 secs

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: May 30, 2006, 09:59:07 ; Search time 67.333 Seconds
(without alignments)
206.068 Million cell updates/sec

Title: US-10-758-165A-3
Perfect score: 74
Sequence: 1 RNNVLIGTDQDQATTR 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues
Total number of hits satisfying chosen parameters: 8966

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 7.2:*
1: uniprot_sprot:*
2: uniprot_crembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	33.8	15	1	NIFS1_ANAVA
2	24	32.4	15	2	Q9S8D5_CYNCA
3	23	31.1	14	2	Q4XS12_PLACH
4	22	29.7	9	2	P70740_RALEU
5	22	29.7	12	2	Q9WZS4_CANFA
6	22	29.7	14	2	Q9TR07_BOVIN
7	22	29.7	15	2	Q9TRH1_BOVIN
8	21	28.4	10	2	Q6UDW9_CANFA
9	21	28.4	13	2	Q75MV9_HUMAN
10	21	28.4	14	2	P83330_STRTTR
11	21	28.4	15	2	Q29622_RABIT
12	21	28.4	15	2	Q9TR62_RABIT
13	20	27.0	10	1	COX5A_ONCMY
14	20	27.0	10	2	Q9U046_HUMAN
15	20	27.0	15	2	Q6WZ21_HUMAN
16	20	27.0	15	2	Q5GJH2_COXBU
17	20	27.0	15	2	Q5GJH9_COXBU
18	19	25.7	8	2	Q1LVG5_TAROF
19	19	25.7	8	2	Q9SB24_TOBAC
20	19	25.7	10	2	Q53X10_POVBK
21	19	25.7	10	2	Q53X11_POVBK
22	19	25.7	10	2	Q53X32_POVBK
23	19	25.7	10	2	Q53X33_POVBK
24	19	25.7	10	2	Q76V79_9POLY
25	19	25.7	11	1	RANC_RANPI
26	19	25.7	11	2	Q06626_SOLTU
27	19	25.7	11	2	Q5EDJ3_LEGPN
28	19	25.7	13	1	FR12_PEA
29	19	25.7	13	1	Q7M4P7_HUMAN
30	19	25.7	13	2	Q9SB03_ORYSA
31	19	25.7	13	2	Q6RSN3_COXBU

32	19	25.7	14	2	Q9P0W1_HUMAN
33	19	25.7	14	2	Q714T6_PSEUK
34	19	25.7	14	2	Q811Y9_PCYAN
35	19	25.7	15	1	TX11B_BUNCA
36	19	25.7	15	2	Q9UR90_YEAST
37	19	25.7	15	2	P82936_HORVU
38	19	25.7	15	2	Q8WK21_9STRA
39	18	24.3	9	2	Q7M2N7_BOSIN
40	18	24.3	9	2	Q4QWV3_9MARC
41	18	24.3	9	2	Q4QWV9_9MARC
42	18	24.3	9	2	Q9JH81_HHV8
43	18	24.3	10	1	COICIN_PSHCN
44	18	24.3	10	1	CWP14_LYCES
45	18	24.3	10	2	Q4QWV8_9MARC

ALIGNMENTS

```

RESULT 1
ID NIFS1_ANAVA STANDARD: PRT; 15 AA.
AC Q44507;
DT 27-APR-2001, integrated into UniProtKB/Swiss-Prot.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 31.
DE Cysteine desulfurase 1 (EC 2.8.1.7) (Nitrogenase metalloclusters
DE biosynthesis protein nifs1) (Fragment).
GN Name=nifs1; Synonyms=nifs;
OS Anabaena variabilis.
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX NCBI_Taxid=1172;
RN [1]
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RC STRAIN=PCC 7937 / ATCC 29413;
RA Monnerjahn U., Boehme H.;
RL Submitted (DEC-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP EXPRESSION PATTERN.
RC STRAIN=PCC 7937 / ATCC 29413;
RX MEDLINE=96016168; PubMed=7568132;
RA Thiel T., Lyons E.M., Erker J.C., Ernst A.;
RL "A second nitrogenase in vegetative cells of a heterocyst-forming
RT cyanobacterium."
RL Proc. Natl. Acad. Sci. U.S.A. 92:9358-9362(1995).
CC -!- FUNCTION: Catalyzes the removal of elemental sulfur atoms from
CC cysteine to produce alanine. Seems to participate in the
CC biosynthesis of the nitrogenase metalloclusters by providing the
CC inorganic sulfur required for the Fe-S core formation (By
CC similarity).
CC -!- CATALYTIC ACTIVITY: L-cysteine + [enzyme]-cysteine = L-alanine +
CC (enzyme)-S-sulfanylcysteine.
CC -!- COFACTOR: Pyridoxal phosphate (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- MISCELLANEOUS: Belongs to the NifH gene cluster which is expressed
CC in heterocysts under anaerobic and aerobic conditions.
CC -!- SIMILARITY: Belongs to the class-V pyridoxal-phosphate-dependent
CC aminotransferase family. Nifs1/scs subfamily.
CC
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CC
DR EMBL, X69898; CAA49523.1; -; Genomic_DNA.
DR PIR, S32677; S32677.
DR InterPro, IPR000192; Aminoacids V.
DR PROSITE, PS00595; AA_TRANSFERRIN CLASS 5; PARTIAL.
KW Nitrogen fixation; Pyridoxal phosphate; Transferrase.
FT CHAIN 1 >15
FT Cysteine desulfurase 1.
FT FTID=PRO_0000150248.
SQ SEQUENCE 15 AA; 1684 MW; 08B8F106DE5547D CRC64;
Query Match 33.8%; Score 25; DB 1; Length 15;

```

Best Local Similarity 45.5%; Pred. No. 1.8e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 5 LIQTDQATTR 15
: | | | |
Db 3 VIVLDNNATTK 13

RESULT 2

ID Q9S8D5_CYNCA PRELIMINARY; PRT; 15 AA.
AC Q9S8D5;

DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.

DT 07-FEB-2006, entry version 11.
DE CARDOSIN A (Fragment).

OS Cynara cardunculus (Cardoon).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; campanulids; Asterales; Asteraceae; Carduoideae; Cardueae;

OC Cynara.
NCBI_TaxID=4265;

CC
RN NCBI_TaxID=4265;
RX [1]

RP PROTEIN SEQUENCE.
RX MEDLINE=96073661; PubMed=8540346;

RA Faro C., Verissimo P., Lin Y., Tang J., Pires E.;
RL "Cardosin A and B, aspartic proteases from the flowers of cardoon.";

Adv. Exp. Med. Biol. 362:373-377(1995).
CC -----

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CC
SQ SEQUENCE 15 AA; 1555 MW; CC95D9155C97325B CRC64;

Query Match 32.4%; Score 24; DB 2; Length 15;
Best Local Similarity 36.4%; Pred. No. 2.9e+03;

Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 3 NVLIQTDQAT 13
: | | | |
Db 4 SAIVATDQNT 14

RESULT 3

ID Q4XS12_PLACH PRELIMINARY; PRT; 14 AA.
AC Q4XS12;

DT 05-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2005, sequence version 1.

DT 07-FEB-2006, entry version 4.
DE Hypothetical protein (Fragment).

GN ORFNames=RC106890.00.0;
OS Plasmodium chabaudi.

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5825;

CC
OX NCBI_TaxID=5825;
RN [1]

RP NUCLEOTIDE SEQUENCE.
RX PubMed=15637271; DOI=10.1126/science.1103717;

RA Hall N., Karras M., Raine J.D., Carlton J.M., Kool J.T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,

RA James K., Rutherford K., Harris B., Harris D., Churcher C.M.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,

RA Biwell S.L., Rajandream M.A., Carucci D.J., Yates J.R. III,
RA Karates F.C., Janse C.J., Barrell B.G., Turner C.M.R., Waters A.P.,

RA Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";

RL Science 307:82-86(2005).
CC -----

CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC preliminary data.

CC -----
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CC EMBL; CAJ01003511; CAH80130.1; -, Genomic_DNA.

KM Hypothetical protein.
FT NON_TER 1

SQ SEQUENCE 14 AA; 1781 MW; 989A795983FA9A51 CRC64;

Query Match 31.1%; Score 23; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 4.1e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 NNVLIQ 7
: | | | |
Db 8 NNVLIFQ 13

RESULT 4

ID P70740_RALEU PRELIMINARY; PRT; 9 AA.
AC P70740;

DT 01-FEB-1997, integrated into UniProtKB/TrEMBL.
DT 01-FEB-1997, sequence version 1.

DT 07-FEB-2006, entry version 18.
DE Hoxa protein (Fragment).

GN Name=hoxa;
OS Rattus norvegicus (Rat).

OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Cupriavidus.

NCBI_TaxID=106590;
CC [1]

RP NUCLEOTIDE SEQUENCE.
RX STRAIN=H16;

RA Lenz O., Schwartz E., Darnedde J., Bitinger M., Friedrich B.;
RT "The Alcaligenes eutrophus H16 hoxa gene participates in hydrogenase

regulation.";
RL J. Bacteriol. 176:4385-4393(1994).

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CC
SQ SEQUENCE 9 AA; 992 MW; 970BD1ADC6D33AB5 CRC64;

Query Match 29.7%; Score 22; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+06;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 8 TDQQT 13
: | | | |
Db 2 SDQQT 7

Db 2 SDQQT 7

Db 2 SDQQT 7

RESULT 5

ID G9MZS4_CANFA PRELIMINARY; PRT; 12 AA.
AC G9MZS4;

DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.

DT 07-FEB-2006, entry version 8.
DE Growth hormone (Fragment).

OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.

NCBI_TaxID=9615;
CC [1]

RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22319383; PubMed=12431806; DOI=10.1016/S0303-7207(02)00257-5;

RA Lantinga-van Leeuwen I.S., Timmermans-Sprang E.A., Mol J.A.;
RT "Cloning and characterization of the 5'-flanking region of the canine

growth hormone gene.";

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RL Mol. Cell. Endocrinol. 197:133-141(2002).
CC -----
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CC Distributed under the Creative Commons Attribution-NonDerivs License
CC
DR EMBL: AF166119; AAF89582.1; -; Genomic_DNA.
FT NON_TER 12 12 1229 MW; 2B587268BCB45417 CRC64;
SQ SEQUENCE 12 AA; 1447 MW; C8322EB96DD9C6C6 CRC64;

Query Match 29.7%; Score 22; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 5.4e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 RNNVLI 6
   |||:|
Db 6 RNSVLL 11

RESULT 6
Q9TRQ7_BOVIN PRELIMINARY; PRT; 14 AA.
AC Q9TRQ7;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Calcyclin-associated protein peptide L-8, CAP-50=ANNEXIN (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP PROTEIN SEQUENCE.
RA MEDLINE=92317074; PubMed=1618851;
RA Mizutani A., Usuda N., Tokumitsu H., Minami H., Yasui K.,
RA Kobayashi R., Higaki H.;
RT "CAP-50, a newly identified annexin, localizes in nuclei of cultured
RT fibroblast 3T1 cells.";
RL J. Biol. Chem. 267:13498-13504(1992).
CC -----
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CC
DR EMBL: AY514688; AAT44872.1; -; Genomic_DNA.
FT NON_TER 1 14 14 MW; C8322EB96DD9C6C6 CRC64;
FT NON_TER 1 14 14 MW; C8322EB96DD9C6C6 CRC64;
SQ SEQUENCE 14 AA; 1447 MW; C8322EB96DD9C6C6 CRC64;

Query Match 29.7%; Score 22; DB 2; Length 14;
Best Local Similarity 80.0%; Pred. No. 6.4e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 TDQQA 12
   |||:|
Db 4 TDEQA 8

RESULT 7
Q9TRH1_BOVIN PRELIMINARY; PRT; 15 AA.
AC Q9TRH1;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 11.
DE Alkaline phosphodiesterase I (EC 3.1.4.1) (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP PROTEIN SEQUENCE.
RA MEDLINE=93250579; PubMed=8387370;
RA Matryama E., Iwamatsu A., Takashima S.;

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RL Biochem. Mol. Biol. Int. 29:579-586(1993).
CC -----
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CC
DR GO: 0004528; F:phosphodiesterase I activity; IEA.
SQ SEQUENCE 15 AA; 1678 MW; BE31498BEA8B7071 CRC64;

Query Match 29.7%; Score 22; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 6.9e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 VLIQTQDQAT 13
   |||:|
Db 2 VLIQTQWQST 11

RESULT 8
O6UDM9_CANFA PRELIMINARY; PRT; 10 AA.
AC O6UDM9;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Mitochondrial H+ transporting ATP synthase F1 (Fragment).
GN Name=ATP5A1;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA PubMed=15233990; DOI=10.1016/j.ygeno.2004.04.001;
RA Houley D.J.E., Ritzert E., Venta P.J.;
RT "Comparative radiation hybrid map of canine chromosome 1 (CFA1)
RT incorporating SNP and indel polymorphisms.";
RL Genomics 84:248-264(2004).
CC -----
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CC
DR EMBL: AY514688; AAT44872.1; -; Genomic_DNA.
FT NON_TER 1 10 10 MW; C47457B1A045B042 CRC64;
FT NON_TER 1 10 10 MW; C47457B1A045B042 CRC64;
SQ SEQUENCE 10 AA; 1059 MW; C47457B1A045B042 CRC64;

Query Match 28.4%; Score 21; DB 2; Length 10;
Best Local Similarity 55.6%; Pred. No. 6.7e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 NVLIQTQDQ 11
   |||:|
Db 2 NVLSITDQ 10

RESULT 9
O7SMV9_HUMAN PRELIMINARY; PRT; 13 AA.
AC O7SMV9;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 21-FEB-2006, entry version 8.
DE Hypothetical protein SSBP1 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=22737999; PubMed=12653948; DOI=10.1038/nature01782;

```

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RA Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
RA Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,
RA Wylie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.E.,
RA Powell G.A., Delenauity K.D., Miner T.L., Nash W.E., Cordes M., Du H.,
RA Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,
RA Vabnick A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,
RA Ozerovskiy P., Belicki L., Scott K., Holmes A., Harkins R., Harris A.,
RA Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,
RA Kozlovicz-Reilly A., Leonard S., Rohlfing T., Rock S.M.,
RA Tin-Wollam A.-M., Abbott A., Mink P., Maupin R., Strommatt C.,
RA Latreille P., Miller N., Johnson D., Murray J., Woessner J.P.,
RA Wendi M.C., Yang S.-P., Schultz B.R., Wallis J.W., Spieth J.,
RA Bieri T.A., Nelson J.O., Berkowicz N., Wohldmann P.E., Cook L.L.,
RA Hickenbotham M.T., Eldred J., Williams D., Bedell J.A., Mardis E.R.,
RA Clifton S.W., Chissole S.L., Marra M.A., Raymond C., Haugen E.,
RA Gillet W., Zhou Y., James R., Phelps K., Iadonoto S., Bubb K.,
RA Simms E., Levy R., Clendenning J., Kaul R., Kent W.J., Frey T.S.,
RA Baertsch R.A., Brent M.R., Keibler E., Flicker P., Bork P., Suyama M.,
RA Bailey J.A., Portnoy M.E., Torrents D., Chinwalla A.T., Gish W.R.,
RA Eddy S.R., McPherson J.D., Olson M.V., Eichler E.E., Green E.D.,
RA Wareton R.H., Wilson R.K.,
RA "The DNA sequence of human chromosome 7."
RT Nature 424:157-164 (2003).
RL [2]
RP NUCLEOTIDE SEQUENCE.
RA Wareton R.,
RP Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
RL [3]
RP NUCLEOTIDE SEQUENCE.
RA Wilson R.,
RP Submitted (JAN-2004) to the EMBL/Genbank/DBJ databases.
CC -----
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CC -----
DR EMBL: AC004979; AAS02037.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON TER
SQ SEQUENCE 13 AA; 1565 MW; 9A39BF645040DAB5 CRC64;

Query Match 28.4%; Score 21; DB 2; Length 13;
Best Local Similarity 37.5%; Pred. No. 9.2e+03;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 NVLIQTDPQ 10
Db 1 NITFLSDQ 8

RESULT 10
P83330_STRTR PRELIMINARY; PRT; 14 AA.
AC P83330;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE M protein, serotype 32 (Fragment).
OS Streptococcus thermophilus.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1308;
RN [1]
RP PROTEIN SEQUENCE.
RC STRAIN=ITCSTR2;
RA Guilford C., Chopard M.A., Gailard J.L., Chamba J.F.,
RT "Comparative study of the protein composition of three strains of
RT Streptococcus thermophilus grown either in M17 medium or in milk."
RL Lait 0:0-0 (2002).
CC -!- FUNCTION: This protein is one of the different antigenic serotypes
CC of protein M. Protein M is closely associated with virulence of
CC the bacterium and can render the organism resistant to
CC phagocytosis (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Cell wall (By

```

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CC similarity).
CC -!- SIMILARITY: TO OTHER M PROTEINS.
CC -!- SIMILARITY: TO OTHER STREPTOCOCCAL AND STAPHYLOCOCCAL PROTEINS IN
CC THE REGION OF THE MEMBRANE ANCHOR.
CC -----
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CC -----
DR GO: GO:0005618; C:cell wall; IEA.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0009405; P:phagocytosis; IEA.
DR GO: GO:0006909; P:phagocytosis; IEA.
KW Antigen; Cell wall; Phagocytosis; Transmembrane; Virulence.
FT NON TER
FT NON TER
SQ SEQUENCE 14 AA; 1739 MW; 66339BF3A3FE24B CRC64;

Query Match 28.4%; Score 21; DB 2; Length 14;
Best Local Similarity 28.6%; Pred. No. 1e+04;
Matches 4; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 2 NVLIQTDPQATTR 15
Db 1 NHOULTQENERLTK 14

RESULT 11
Q29622_RABIT PRELIMINARY; PRT; 15 AA.
AC Q29622;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 2.
DT 07-FEB-2006, entry version 23.
DE Recombination activating protein (Fragment).
GN Name=RAG-2;
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=RIM/rqm; TISSUE=Thymus;
RX MEDLINE=93354283; PubMed=8350872; DOI=10.1016/0161-5890(93)90127-W;
RA Fuschioti P., Hardranath N., Mage R.G., McCormack W.T.,
RA Dhanarajan P., Roux K.H.,
RT "Recombination activating genes-1 and -2 of the rabbit: cloning and
RT characterization of germline and expressed genes."
RL Mol. Immunol. 30:1021-1032 (1993).
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CC -----
DR EMBL: M99310; AAA03028.1; -; mRNA.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0003677; F:DNA binding; IEA.
DR GO: GO:0006310; P:DNA recombination; IEA.
DR InterPro: IPR004321; RAG2.
DR Pfam: PF03089; RAG2; 1.
FT NON TER
FT NON TER
SQ SEQUENCE 15 AA; 1717 MW; CE095FAD5F7ED42B CRC64;

Query Match 28.4%; Score 21; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RNNVLI 6
Db 9 RNNIAL 14

RESULT 12
Q9TR62_RABIT

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ID 09TR62_RABIT PRELIMINARY; PRT; 15 AA.
AC 09TR62;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
QY 07-FEB-2006, entry version 9.
DE Apolipoprotein A-IV (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=95329112; PubMed=7605356; DOI=10.1016/0021-9150(94)05444-N;
RA Mezdour H., Yamamura T., Nomura S., Yamamoto A.;
RT "Genetic but not diet-induced hypercholesterolemia causes low
RT apolipoprotein A-IV level in rabbit sera.";
RL Atherosclerosis 113:171-178(1995).
-----
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CC
SQ SEQUENCE 15 AA; 1761 MW; DE115B7351F0ABC CRC64;

Query Match 28.4%; Score 21; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.1e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 IQTDOQT 13
: |||
Db 2 VSADQVAT 9

RESULT 13
COXS3A ONCMY STANDARD; PRT; 10 AA.
AC P80328;
DT 01-OCT-1994, integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-1994, sequence version 1.
DT 07-FEB-2006, entry version 27.
DE Cytochrome c oxidase polypeptide Va, mitochondrial (EC 1.9.3.1)
DE (Fragment).
OS Oncoerythrus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncoerythrus.
OX NCBI_TaxID=8022;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=94237150; PubMed=8181469;
RA Freund R., Kadenbach B.;
RT "Identification of tissue-specific isoforms for subunits Vb and Vlla
RT of cytochrome c oxidase isolated from rainbow trout.";
RL Bur. J. Biochem. 221:1111-1116(1994).
CC -1- FUNCTION: This is the heme A-containing chain of cytochrome c
CC oxidase, the terminal oxidase in mitochondrial electron transport.
CC -1- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
CC c + 2 H(2)O.
CC -1- SUBCELLULAR LOCATION: Mitochondrion; mitochondrial inner membrane.
CC -1- SIMILARITY: Belongs to the cytochrome c oxidase Va family.
-----
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CC
PIR: S43625; S43625.
KM Direct protein sequencing; Heme; Inner membrane; Iron; Membrane;
KM Metal-binding; Mitochondrion; Oxidoreductase.
FT CHAIN 1 >10 Cytochrome c oxidase polypeptide Va.
/FTID=PRO_0000195214.
FT
NON TER 10 10
SEQUENCE 10 AA; 1144 MW; CS35CSB1AB02C33D CRC64;

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Query Match 27.0%; Score 20; DB 1; Length 10;
Best Local Similarity 33.3%; Pred. No. 1.1e+04;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 6 IQTDOQ 11
: |||
Db 5 VETDEE 10

RESULT 14
Q9UJ48_HUMAN PRELIMINARY; PRT; 10 AA.
ID Q9UJ48_HUMAN
AC Q9UJ48;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE Lactophilin-2 (Fragment).
GN Name=LPHN1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99153747; PubMed=10030676; DOI=10.1038/sj.onc.1202487;
RA White G.R.M., Varley J.M., Heighway J.;
RT "Isolation and characterisation of a human homologue of the
RT lactophilin gene from a region of 1p31.1 implicated in breast
RT cancer.";
RL Oncogene 17:3513-3519(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20225451; PubMed=10760572; DOI=10.1016/S0167-4781(00)00020-8;
RA White G.R.M., Varley J.M., Heighway J.;
RT "Genomic structure and expression profile of LPHN1, a 7TM gene
RT variably expressed in breast cancer cell lines.";
RL Biochim. Biophys. Acta 1491:75-92(2000).
-----
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CC
DR EMBL: AJ244514; CAB60206.1; Genomic DNA.
FT
NON TER 1 1
SEQUENCE 10 AA; 1112 MW; 06CC4C2720544724 CRC64;

Query Match 27.0%; Score 20; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 NVLIQ 7
: |||
Db 5 NILIQ 9

RESULT 15
Q6MZZ1_HUMAN PRELIMINARY; PRT; 15 AA.
ID Q6MZZ1_HUMAN
AC Q6MZZ1;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Hypothetical protein DKFZp686J2076.
GN Name=DKFZp686J2076;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Human endometrium carcinoma cell line;
RG The German Human cDNA Consortium;

```

RA Ansoorge W., Krieger S., Regiert T., Ritzmuller C., Schwager B.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.,
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL: BX640801; CAB35884.1; -; mRNA.
KW Hypothetical protein.
SQ SEQUENCE 15 AA; 1715 MW; 91F5CE0118445CE3 CRC64;

Query Match 27.0%; Score 20; DB 2; Length 15;
Best Local Similarity 42.9%; Pred. No. 1.7e+04;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 LIQTDQ 11
|:|:
|:|:
Db 4 LKVDQE 10

Search completed: May 30, 2006, 11:10:01
Job time : 69.333 secs

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OM protein - protein search, using sw model

```
Run on:      May 30, 2006, 09:58:50 ; Search time 60 Seconds
              (without alignments)
              114.304 Million cell updates/sec
```

Title:	US-10-758-165A-3
Perfect score:	74
Sequence:	1 RNNVLIQTDDQATTR 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 837126

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Minimum DB seq length: 0
Maximum DB seq length: 15
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *
9: geneseqp2005s: *
10: geneseqp2006s: *

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	74	100.0	15	8	ADRI0603	Adri0603 Horse IGF1
2	49	66.2	15	7	ADCE64568	AdCE64568 Horse Imm
3	41	55.4	15	8	ADRI0601	Adri0601 Dog IGE
4	40	54.1	15	8	ADRI0607	Adri0607 Pig IGE
5	37	50.0	15	8	ADRI0602	Adri0602 Cat IGE
6	32	43.2	15	7	ADDA4095	AdDA4095 CP2 peptide
7	32	43.2	15	7	ADDA4240	AdDA4240 Carboxypep
8	29	39.2	12	9	AEC11192	Aec11192 Pseudomon
9	29	39.2	15	3	AAV65622	AAV65622 Oestrogen
10	29	39.2	15	5	PAU86359	PAU86359 Oestrogen
11	29	39.2	15	8	ADM79070	ADM79070 Oestrogen
12	29	39.2	15	8	ADRI0604	Adri0604 Sheep IGF1
13	28	37.8	15	9	AEC98485	Aec98485 HLA-DR b1
14	28	37.8	15	9	AEC98272	Aec98272 HLA-DR b1
15	27	36.5	11	4	AAV95534	AAV95534 Human com
16	27	36.5	11	9	ADV57215	Adv57215 G protein
17	27	36.5	11	9	ADVS4438	AdvS4438 G protein
18	27	36.5	11	9	ADVS6449	AdvS6449 G protein
19	27	36.5	13	7	ADDA4391	AdDA4391 CP2 peptide
20	27	36.5	14	4	AAB72622	AAb72622 Human H1L
21	27	36.5	15	5	ABG72874	ABg72874 Human RalA
22	27	36.5	15	7	ADDA4241	AdDA4241 Carboxypep
23	27	36.5	15	8	ADNT1414	AdnT1414 Human 2733

25	27	36.5	15	8	ADN71546	Adt71546	Human	273
25	27	36.5	15	8	ADN71055	Adt71055	Human	273
26	27	36.5	15	8	ADN70693	Adt70693	Human	273
27	27	36.5	15	8	ADN70579	Adt70579	Human	273
28	27	36.5	15	8	ADN71415	Adt71415	Human	273
29	26	35.1	9	9	AED61860	Aed61860	Chlorocox	
30	26	35.1	10	8	AD112489	Ad112489	Scorpiox	
31	26	35.1	10	8	ADH89500	Adh89500	Scorpion	
32	26	35.1	12	9	ADY55643	Ady55643	Hair-bind	
33	26	35.1	12	9	AED49042	Aed49042	Dust mite	
34	26	35.1	12	9	AED55089	Aed55089	Hair-bind	
35	26	35.1	13	7	ADD43993	Ad43993	CPG2 pept	
36	26	35.1	15	5	ABP57763	Abp57763	Human pho	
37	26	33.8	9	8	ADN67893	Adn67893	Human	273
38	25	33.8	9	8	ADN67646	Adn67646	Human	273
39	25	33.8	9	8	ADN68615	Adn68615	Human	273
40	25	33.8	9	8	ADN69336	Adn69336	Human	273
41	25	33.8	9	8	ADN68418	Adn68418	Human	273
42	25	33.8	10	8	ADN70395	Adt70395	Human	273
43	25	33.8	10	8	ADN69955	Adn69955	Human	273
44	25	33.8	10	8	ADN69607	Adt69607	Human	273
45	25	33.8	12	4	ADU17678	Adu17678	Novel	sig

ALIGNMENTS

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RESULT 1
ADR10603
ID   ADR10603 standard; peptide; 15 AA
..

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21-OCT-2004 (first entry)

KW Antiasthmatic; Antiallergic; Immunosuppressive; IGE; dog; asthma;
 KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
 KW horse.

OS	Equus caballus.
XX	
PN	WO2004065936-A2.

(UYNC-) UNIV NORTH CAROLINA STATE
Hammerberg B;
WPI; 2004-593545/57.

PT Novel antibody that specifically binds to mammalian IgE epitope, useful
PT for testing an allergen reactivity of IgE sample, detecting mammalian IgE
PT or treating asthma or anaphylactic shock.

Example 6; Page 9; 14pp; English.

The present invention relates to novel monoclonal antibody (1) that specifically binds to a mammalian IgE epitope, where the epitope is between amino acids 145-166 or 356-374 of mammalian IgE, e.g. dog IgE. (1) is useful for testing an allergen reactivity of an IgE sample. The allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut and corn allergens. The sample is a biological sample collected from a dog, cat or horse. (1) is also useful for detecting mammalian IgE and for treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal antibodies recognise epitopes on canine IgE corresponding to amino acid residues 357-371 (ABDr10601) and 146-162 (ABDr10603) respectively of the

CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with
 CC either pig or human epsilon-chains of IGE. The present sequence is the
 CC horse IGE 5.91 recognition site.
 CC
 XX

SQ Sequence 15 AA;

Query Match 100.0%; Score 74; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 2.1e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RNNVLIOFDQOATTR 15
 |||||
 1 RNNVLIOFDQOATTR 15

Db 1 RNNVLIOFDQOATTR 15

RESULT 2

ADC64568
 ID ADC64568 standard; peptide; 15 AA.

AC ADC64568;

DT 18-DEC-2003 (first entry)

DE Horse immunoglobulin E, IGE, heavy chain immunogenic peptide P4.

XX Horse; immunoglobulin E, IGE; heavy chain; immunogen; allergy.

KW Equus caballus.

OS US2003087314-A1.

XX 08-MAY-2003.

XX 08-NOV-2001; 2001US-00052788.

XX 08-NOV-2001; 2001US-00052788.

XX (REGC) UNIV CALIFORNIA.

XX Gershwin LJ, Pettigrew HD, Kalina WV;

XX WPI; 2003-765437/72.

PT Immunogenic composition comprising an isolated equine immunoglobulin E
 PT polypeptide that induces production of antibodies which specifically bind
 PT to equine immunoglobulin E.
 XX

PS Example 1; Page 8; 14pp; English.

CC The invention relates to an immunogenic composition comprising an
 CC isolated polypeptide having an amino acid sequence that is at least 80%
 CC identical to 6 (SI-56), 15 amino acid peptide sequences derived from
 CC equine immunoglobulin E (the composition induces production of an
 CC antibody that specifically binds to equine immunoglobulin (Ig)E), the six
 CC polypeptides are not explicitly identified in the specification. Also
 CC included are a composition comprising an antibody that specifically binds
 CC to a polypeptide at least 80% identical to (SI)-(56), an antibody that
 CC specifically binds to equine IGE made by the process of immunising an
 CC animal with a polypeptide at least 80% identical to (SI)-(56), making an
 CC antibody that specifically binds to equine IGE (involving immunising an
 CC animal with a composition further comprising an isolated polypeptide (the
 CC amino acid sequence of the polypeptide is at least 80% identical to (SI)-
 CC (56)), and collecting antiserum from the animal) and a kit for detection
 CC of equine IGE in a biological sample comprising the antibody and means
 CC for detecting specific binding of the antibody to equine IGE. The
 CC antibody is useful for detecting equine IGE protein in a biological
 CC sample (serum) which involves contacting the sample with the antibody,
 CC thus forming an antigen/antibody complex, and detecting the presence or
 CC absence of the antigen/antibody complex. The antibody and antigen are
 CC immobilised on a solid surface. The antibody is labelled such that the

CC complex can be detected. The complex is detected using a second labelled
 CC antibody. The peptides are useful for generating antibodies specific for
 CC IGE which can serve as a diagnostic test for allergy. The present
 CC sequence is a Horse immunoglobulin E, IGE, heavy chain immunogenic
 CC peptide from the early portion of the C4 region.
 CC
 XX

SQ Sequence 15 AA;

Query Match 66.2%; Score 49; DB 7; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.074;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 IQTDOQATTR 15
 |||||
 1 IQTDOQATTR 10

Db 1 IQTDOQATTR 10

RESULT 3

ADR10601
 ID ADR10601 standard; peptide; 15 AA.

AC ADR10601;

DT 21-OCT-2004 (first entry)

DE Dog IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 1.

XX Antiaesthetic; Anti-allergic; Immunosuppressive; IGE; dog; asthma;

KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody.

XX Canis familiaris.

OS WO2004065936-A2.

XX 05-AUG-2004.

XX 15-JAN-2004; 2004WO-US003566.

XX 16-JAN-2003; 2003US-0440472P.

XX (UNNC-) UNIV NORTH CAROLINA STATE.

XX Hammerberg B;

XX WPI; 2004-593545/57.

PT Novel antibody that specifically binds to mammalian IGE epitope, useful
 PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE
 PT or treating asthma or anaphylactic shock.
 XX

PS Example 6; Page 9; 14pp; English.

CC The present invention relates to a novel monoclonal antibody (I) that
 CC specifically binds to a mammalian IGE epitope, where the epitope is
 CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
 CC (I) is useful for testing an allergen reactivity of an IGE sample. The
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
 CC and corn allergens. The sample is a biological sample collected from a
 CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
 CC antibodies recognise epitopes on canine IGE corresponding to amino acid
 CC residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the
 CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with
 CC either pig or human epsilon-chains of IGE.
 CC
 XX

SQ Sequence 15 AA;

Query Match 55.4%; Score 41; DB 8; Length 15;
 Best Local Similarity 64.3%; Pred. No. 2.1;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RNNVLQTDQOATT 14
 ||: |||||
 DB 1 RNDSPQTDQYTTT 14

RESULT 4

ID ADR10607 standard; peptide; 15 AA.

AC ADR10607;

DT 21-OCT-2004 (first entry)

DE Pig IgE epitope recognised by monoclonal antibody 5.91, SEQ ID 7.

KM Antiasthmatic; Antiallergic; Immunosuppressive; IgE; dog; asthma;
 KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
 KM pig.

OS Sub scrofa.

PN WO2004065936-A2.

XX 05-AUG-2004.

PF 15-JAN-2004; 2004WO-US003566.

PR 16-JAN-2003; 2003US-0440472P.

XX (UYN-) UNIV NORTH CAROLINA STATE.

PA Hammerberg B;

PI WPI; 2004-593545/57.

DR Novel antibody that specifically binds to mammalian IgE epitope, useful
 PT for testing an allergen reactivity of IgE sample, detecting mammalian IgE
 PT or treating asthma or anaphylactic shock.

XX Example 6; Page 9; 14pp; English.

CC The present invention relates to a novel monoclonal antibody (I) that
 CC specifically binds to a mammalian IgE epitope, where the epitope is
 CC between amino acids 145-166 or 356-374 of mammalian IgE, e.g. dog IgE.
 CC (I) is useful for testing an allergen reactivity of an IgE sample. The
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
 CC and corn allergens. The sample is a biological sample collected from a
 CC dog, cat or horse. (I) is also useful for detecting mammalian IgE and for
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
 CC antibodies recognise epitopes on canine IgE corresponding to amino acid
 CC residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the
 CC canine IgE epsilon-chain. Recognition of epsilon-chains from IgE from
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
 CC of IgE from cat and horse, but did not exhibit cross-reactivity with
 CC either pig or human epsilon-chains of IgE. The present sequence is the
 CC pig IgE 5.91 recognition site.

XX Sequence 15 AA;

Query Match 54.1%; Score 40; DB 8; Length 15;
 Best Local Similarity 46.7%; Pred. No. 3.3;
 Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 RNNVLQTDQOATT 15
 ||: |||||

DB 1 RNDAPVQADRHSTTR 15

RESULT 5
 ADR10602
 ID ADR10602 standard; peptide; 15 AA.

XX ADR10602;

XX 21-OCT-2004 (first entry)

DE Cat IgE epitope recognised by monoclonal antibody 5.91, SEQ ID 2.

KM Antiasthmatic; Antiallergic; Immunosuppressive; IgE; dog; asthma;
 KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
 KM cat.

OS Fells catus.

PN WO2004065936-A2.

XX 05-AUG-2004.

PF 15-JAN-2004; 2004WO-US003566.

PR 16-JAN-2003; 2003US-0440472P.

XX (UYN-) UNIV NORTH CAROLINA STATE.

PA Hammerberg B;

PI WPI; 2004-593545/57.

DR Novel antibody that specifically binds to mammalian IgE epitope, useful
 PT for testing an allergen reactivity of IgE sample, detecting mammalian IgE
 PT or treating asthma or anaphylactic shock.

XX Example 6; Page 9; 14pp; English.

CC The present invention relates to a novel monoclonal antibody (I) that
 CC specifically binds to a mammalian IgE epitope, where the epitope is
 CC between amino acids 145-166 or 356-374 of mammalian IgE, e.g. dog IgE.
 CC (I) is useful for testing an allergen reactivity of an IgE sample. The
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
 CC and corn allergens. The sample is a biological sample collected from a
 CC dog, cat or horse. (I) is also useful for detecting mammalian IgE and for
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
 CC antibodies recognise epitopes on canine IgE corresponding to amino acid
 CC residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the
 CC canine IgE epsilon-chain. Recognition of epsilon-chains from IgE from
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
 CC of IgE from cat and horse, but did not exhibit cross-reactivity with
 CC either pig or human epsilon-chains of IgE. The present sequence is the
 CC cat IgE 5.91 recognition site.

XX Sequence 15 AA;

Query Match 50.0%; Score 37; DB 8; Length 15;
 Best Local Similarity 53.8%; Pred. No. 11;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 NNNVLQTDQOATT 14
 ||: |||||

DB 2 NDSPVRTQOATT 14

RESULT 6

ADD44095
 ID ADD44095 standard; peptide; 15 AA.

AC ADD44095;

DT 15-JAN-2004 (first entry)

DE CPG2 peptide #1 able to stimulate human T-cells in vitro.

KW bacterial enzyme; carboxypeptidase G2; CPG2; non-immunogenic;
 immunogenic; T-cell epitope; MHC class II binding ligand;

KW	immunostimulant; enzyme therapy; immune response;
KW	gene directed enzyme prodng strategy; vaccine; enzyme; EC 3.4.17.11.
XX	
XX	Pseudomonas sp. RS-16.
OS	
PN	WO2003045426-A1.
XX	
XX	05-JUN-2003.
PD	
PF	27-NOV-2002; 2002WO-EP013351.
XX	
PR	29-NOV-2001; 2001EP-00128519.
PR	25-JAN-2002; 2002EP-00001778.
XX	
PR	13-SEP-2002; 2002EP-00020634.
XX	
PA	(MERE) MERCK PATENT GMBH.
XX	
PI	Hellendoorn K, Baker M, Williams S, Carr FJ;
DR	WPI; 2003-513617/48.
XX	
PT	New modified bacterial enzyme carboxypeptidase G2 (CPG2) having
PT	substantially non-immunogenic or less immunogenic than any non-modified
CPG2, useful for inducing an immune response in a human host.	
XX	
PS	Claim 3; Page 14; 52pp; English.
XX	
CC	The invention relates to a novel modified bacterial enzyme
CC	carboxypeptidase G2 (CPG2). The modified enzyme can result in CPG2
CC	proteins that are substantially non-immunogenic or less immunogenic than
CC	any non-modified CPG2 having essentially the same biological specificity
CC	when used in vivo, and comprising specific amino acid residues having
CC	alterations compared with the non-modified parental enzyme. The
CC	alterations cause a reduction or an elimination of one or more of T-cell
CC	epitope sequences, which act in the parental enzyme as MHC class II
CC	binding ligands and stimulate T-cells. The modified CPG2 enzyme and the
CC	CPG2 proteins have immunostimulant activity and may be used in enzyme
CC	therapy. The modified CPG2 enzyme may be used to induce an immune
CC	response in a human host, or as a therapeutic entity such as the gene
CC	directed enzyme prodng strategy. The peptide is useful for the
CC	manufacture of a modified CPG2 enzyme having substantially no or less
CC	immunogenicity than any non-modified parental enzyme when used in vivo,
CC	and for vaccination of patients to reduce immunogenicity to CPG2 in vivo.
CC	This sequence represents a CPG2 enzyme peptide able to stimulate human T-
CC	cells in vitro of the invention.
XX	
SO	Sequence 15 AA;
QY	
DB	
Query Match	43.2%; Score 32; DB 7; Length 15;
Best Local Similarity	61.5%; Pred. No. 94;
Matches 8; Conservative	2; Mismatches 1; Indels 2; Gaps 1;
1 RNNVLIQ--TDOQ 11	
1 RNNVLIQ--TDOQ 11	
3 RDNVLEQATDEQ 15	
RESULT 7	
ADDD44240	
ID	ADDD44240 standard; peptide; 15 AA.
XX	
AC	ADD44240;
XX	
DT	15-JAN-2004 (first entry)
XX	
DE	Carboxypeptidase G2 (CPG2) enzyme immunogenic peptide #1.
XX	
KW	bacterial enzyme; carboxypeptidase G2; CPG2; non-immunogenic;
KW	immunogenic; T-cell epitope; MHC class II binding ligand;
KW	immunostimulant; enzyme therapy; immune response;
KW	gene directed enzyme prodng strategy; vaccine; enzyme; EC 3.4.17.11.
OS	Pseudomonas sp. RS-16.

XX	XX	WO2003045426-A1.
XX	PN	
XX	PD	
XX	XX	05-JUN-2003.
XX	XX	
XX	XX	27-NOV-2002; 2002WO-EP013351.
XX	XX	
XX	XX	29-NOV-2001; 2001EP-00128519.
XX	XX	25-JAN-2002; 2002EP-00001778.
XX	XX	13-SEP-2002; 2002EP-00020634.
XX	XX	
XX	PA	(MERE) MERCK PATENT GMBH.
XX	XX	
XX	PI	Hellendoorn K, Baker M, Williams S, Carr FJ;
XX	XX	WPI; 2003-513617/48.
XX	XX	
XX	XX	PT New modified bacterial enzyme carboxypeptidase G2 (CPG2) having
XX	XX	substantially non-immunogenic or less immunogenic than any non-modified
XX	XX	CPG2, useful for inducing an immune response in a human host.
XX	XX	
XX	XX	Example 2; Fig 1; 52pp; English.
XX	XX	
XX	XX	The invention relates to a novel modified bacterial enzyme
XX	XX	carboxypeptidase G2 (CPG2). The modified enzyme can result in CPG2
XX	XX	proteins that are substantially non-immunogenic or less immunogenic than
XX	XX	any non-modified CPG2 having essentially the same biological specificity
XX	XX	when used in vivo, and comprising specific amino acid residues having
XX	XX	alterations compared with the non-modified parochial enzyme. The
XX	XX	alterations cause a reduction or an elimination of one or more of T-cell
XX	XX	epitope sequences, which act in the parental enzyme as MHC class II
XX	XX	binding ligands and stimulate T-cells. The modified CPG2 enzyme and the
XX	XX	CPG2 proteins have immunostimulant activity and may be used in enzyme
XX	XX	therapy. The modified CPG2 enzyme may be used to induce an immune
XX	XX	response in a human host, or as a therapeutic entity such as the gene
XX	XX	directed enzyme prodrug strategy. The peptide is useful for the
XX	XX	manufacture of a modified CPG2 enzyme having substantially no or less
XX	XX	immunogenicity than any non-modified parental enzyme when used in vivo,
XX	XX	and for vaccination of patients to reduce immunogenicity to CPG2 in vivo.
XX	XX	This sequence represents an immunogenic peptide of the CPG2 enzyme of the
XX	XX	invention.
XX	XX	
XX	XX	Sequence 15 AA;
XX	XX	
XX	XX	Query Match 43.2%; Score 32; DB 7; Length 15;
XX	XX	Best Local Similarity 61.5%; Pred. No. 94;
XX	XX	Matches 8; Conservative 2; Mismatches 1; Indels 2; Gaps 1;
XX	XX	
XX	QY	1 RNNVLIQ--TDQ 11
XX	XX	:
XX	XX	:
XX	XX	3 RDNVLFQATDEQ 15
XX	DB	
XX	XX	
XX	XX	RESULT 8
XX	XX	AECL1192
XX	XX	ID AECL1192 standard; peptide; 12 AA.
XX	XX	
XX	XX	AECL1192;
XX	XX	
XX	XX	20-OCT-2005 (first entry)
XX	XX	
XX	XX	Pseudomonas aeruginosa phosphoglucosamine mutase peptide.
XX	XX	
XX	XX	protein purification; antibacterial; antimicrobial; infection;
XX	XX	drug screening; phosphoglucosamine mutase.
XX	XX	
XX	XX	Pseudomonas aeruginosa.
XX	XX	
XX	XX	US2005181388-A1.
XX	XX	
XX	XX	18-AUG-2005.
XX	XX	
XX	XX	04-OCT-2004; 2004US-00958216.
XX	XX	

XX 02-APR-2002; 2002US-0369511P.
PR 04-APR-2002; 2002US-0369817P.
PR 04-APR-2002; 2002US-0370102P.
PR 08-APR-2002; 2002US-0370778P.
PR 08-APR-2002; 2002US-0370792P.
PR 08-APR-2002; 2002US-0370820P.
PR 08-APR-2002; 2002US-0370859P.
PR 08-APR-2002; 2002US-0370899P.
PR 08-APR-2002; 2002US-0371067P.
PR 09-APR-2002; 2002US-0371107P.
PR 09-APR-2002; 2002US-0371140P.
PR 09-APR-2002; 2002US-0371185P.
PR 31-MAY-2002; 2002US-0385089P.
PR 31-MAY-2002; 2002US-0385426P.
PR 04-JUN-2002; 2002US-0385751P.
PR 05-JUN-2002; 2002US-0386018P.
PR 05-JUN-2002; 2002US-0386367P.
PR 05-JUN-2002; 2002US-0386548P.
PR 05-JUN-2002; 2002US-0386553P.
PR 05-JUN-2002; 2002US-0386566P.
PR 05-JUN-2002; 2002US-0386577P.
PR 06-JUN-2002; 2002US-0386283P.
PR 06-JUN-2002; 2002US-0386390P.
PR 06-JUN-2002; 2002US-0386430P.
PR 06-JUN-2002; 2002US-0386430P.
PR 06-JUN-2002; 2002US-0386601P.
PR 06-JUN-2002; 2002US-0386826P.
PR 06-JUN-2002; 2002US-0386869P.
PR 31-JUL-2002; 2002US-0399972P.
PR 01-AUG-2002; 2002US-0400348P.
PR 05-NOV-2002; 2002US-0424053P.
PR 06-NOV-2002; 2002US-0424380P.
PR 06-NOV-2002; 2002US-0424395P.
PR 08-NOV-2002; 2002US-0425200P.
PR 24-DEC-2002; 2002US-0436243P.
PR 24-DEC-2002; 2002US-0436288P.
PR 24-DEC-2002; 2002US-0436345P.
PR 24-DEC-2002; 2002US-0436349P.
PR 26-DEC-2002; 2002US-0436566P.
PR 26-DEC-2002; 2002US-0436567P.
PR 26-DEC-2002; 2002US-0436568P.
PR 27-DEC-2002; 2002US-0436758P.
PR 27-DEC-2002; 2002US-0436708P.
PR 27-DEC-2002; 2002US-0436734P.
PR 27-DEC-2002; 2002US-0436804P.
PR 27-DEC-2002; 2002US-0436834P.
PR 27-DEC-2002; 2002US-0436842P.
PR 27-DEC-2002; 2002US-0436861P.
PR 27-DEC-2002; 2002US-0436885P.
PR 27-DEC-2002; 2002US-0436889P.
PR 27-DEC-2002; 2002US-0436893P.
PR 27-DEC-2002; 2002US-0436900P.
PR 30-DEC-2002; 2002US-0436947P.
PR 30-DEC-2002; 2002US-0436971P.
PR 30-DEC-2002; 2002US-0436987P.
PR 30-DEC-2002; 2002US-0437013P.
PR 30-DEC-2002; 2002US-0437038P.
PR 30-DEC-2002; 2002US-0437141P.
PR 31-DEC-2002; 2002US-0437281P.
PR 31-DEC-2002; 2002US-0437527P.
PR 31-DEC-2002; 2002US-0437620P.
PR 31-DEC-2002; 2002US-0437638P.
PR 02-APR-2003; 2003WO-CA000464.
PR 04-APR-2003; 2003WO-CA000464.
PR 08-APR-2003; 2003WO-CA000481.
PR 08-APR-2003; 2003WO-CA000485.
XX
PA (AFFI-) AFFINIUM PHARM INC.
XX
PI Edwards A, Dharamsi A, Vedadi M, Arrowsmith C, Awrey DE;
PI Beattie B, Buzadzija K, Canadian V, Domagala M, Houston S;

PI Kanagaraiah D, Li Q, Mansoury K, McDonald M, Nethery-Brook K, Ng I;
PI Ouyang H, Pinder B, Richards D, Tai M, Thalakada R, Vallee F;
PI Virag C;
XX
DR WPI, 2005-628189/64.
XX
PT New composition comprising purified polypeptides from bacteria (e.g.
PT Escherichia coli), useful for diagnosing, preventing or treating
PT microbial infections, or in pharmacogenomic or drug screening procedures.
XX
PS Example 1; Fig 219; 667bp; English.
XX
CC The invention relates to a composition (I) comprising purified
CC polypeptides from bacteria. Also described: (1) a crystallized,
CC recombinant polypeptide comprising an amino acid sequence of (I), where
CC the polypeptide is in crystal form; (2) a crystallized complex comprising
CC the crystallized, recombinant polypeptide and a co-factor or a small
CC organic molecule, where the complex is in crystal form; and (3) a host
CC cell comprising a nucleic acid encoding a polypeptide of (I), where a
CC culture of the host cell produces at least about 1 mg of the polypeptide
CC per liter of culture and the polypeptide is at least about one-third
CC soluble as measured by gel electrophoresis. The composition and methods
CC are useful for diagnosing, preventing or treating diseases, such as
CC microbial infections. These may also be used in pharmacogenomic or drug
CC screening procedures. The present sequence represents a Pseudomonas
CC aeruginosa phosphoglucosamine mutase peptide, which is used in an example
CC from the present invention.
XX
SQ Sequence 12 AA:

Query Match 39.2%; Score 29; DB 9; Length 12;
Best Local Similarity 33.3%; Pred. No. 2.6e+02;
Matches 4; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 4 VLQTPDQATTR 15
|::|::|::|
Db 1 VMVSGDEASVR 12

RESULT 9
AAVE5622
ID AAVE5622 standard; peptide; 15 AA.
XX
AC AAVE5622;
XX
DT 01-FEB-2000 (first entry)
XX
DE Oestrogen receptor beta ERK binding peptide 178-beta.
XX
KM Oestrogen receptor; estrogen; estradiol; oestrogen response element; ERK;
KM binding; biological activity; fingerprint; molecular braille;
KM cellular braille; modulation; tamoxifen; breast cancer; ovarian cancer;
KM menopause; osteoporosis; selective oestrogen receptor modulator;
KM identification; characterization; classification.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9954728-A2.
XX
PD 28-OCT-1999.
XX
PF 26-MAR-1999; 99WO-US000664.
XX
PR 23-APR-1998; 98US-0082756P.
PR 09-SEP-1998; 98US-0099656P.
PR 08-JAN-1999; 99US-0115345P.
XX
PA (NOVA-) NOVALON PHARM CORP.
XX
PI Paige LA, Hamilton PT, Fowlkes DM, Buehrer B, Barnett T;
PI McDonnell DP, Christensen DJ;

DR WPI; 2000-013281/01.
 XX Methods for identifying new receptor modulators, especially estrogen
 PT modulators to treat tamoxifen refractory breast cancer.
 PS Example 2.2; Page 164; 219pp; English.
 XX
 CC The present invention describes a method for predicting the biological
 CC activity of new receptor modulating compounds (II) using novel oligomeric
 CC peptides (biokeys) which have differential abilities to bind to 2
 CC different receptor conformations. The method is used to identify new
 CC drugs that are physiological or pharmacological agonists/antagonists and
 CC that target various receptors, which are involved in certain disease
 CC conditions. The system may be used as a primary screening tool to
 CC identify hits, to classify lead compounds from a drug screen to,
 CC characterize selective oestrogen receptor modulators (SERMs) in terms of
 CC agonist and antagonist function and to predict possible clinical effects
 CC of SERMs such as tissue and receptor specificity. The method can also be
 CC applied to the fractionation of mixtures of SERMs to determine which
 CC components are producing agonistic and antagonistic activity. The method
 CC may be used with other receptors (e.g. progesterone, androgen, and
 CC glucocorticoid, thyroid, vitamin D, beta-adrenergic, dopamine and
 CC epidermal growth factor). To identify, characterise and classify
 CC modulators of receptor activity, peptides comprising a LXXLL motif may be
 CC used to modulate the oestrogen receptor in treating e.g. breast and
 CC ovarian cancer and ameliorating the effects of menopause, including
 CC osteoporosis. AA65439 to AA65652 represent oestrogen receptor
 CC estradiol receptor and oestrogen response element binding peptides given
 CC in the exemplification of the present invention. AA235740 to AA235745
 CC represent oligonucleotides used in the exemplification of the present
 CC invention
 CC
 XX
 SQ Sequence 15 AA;
 Query Match 39.2%; Score 29; DB 3; Length 15;
 Best Local Similarity 46.2%; Pred. No. 3.3e+02;
 Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 Oy 3 NVLIQTDOQATTR 15
 Db 3 NLCLCLDOEACSR 15
 RESULT 10
 AAU86359
 ID AAU86359 standard; peptide; 15 AA.
 XX
 AC AAU86359;
 XX
 DT 21-MAY-2002 (first entry)
 XX
 DE Oestrogen receptor beta binding peptide 17E-beta.
 XX
 KM Oestrogen receptor; breast cancer; combinatorial peptide library;
 KM receptor modulating compound.
 XX
 OS Synthetic.
 OS
 PN WO200204956-A2.
 XX
 PD 17-JAN-2002.
 XX
 PF 11-JUL-2001; 2001WO-US021867.
 XX
 PR 12-JUL-2000; 2000US-00614865.
 PR 21-MAY-2001; 2001US-00860688.
 XX
 PA (KARO-) KARO BIO USA INC.
 XX
 PI Fowlkes DM, Barnett TR, Buehrer B;
 XX WPI; 2002-154969/20.
 XX

PT Identifying receptor-binding peptides comprises screening combinatorial
 PT peptide library presented in form of cells each of which coexpress one
 PT peptide member and receptor with signal producing system for reporting
 PT binding.
 PS Disclosure; Page 146; 175pp; English.
 XX
 CC The invention relates to identifying a binding peptide which binds a
 CC receptor and which is a member of a combinatorial library of peptides,
 CC comprising screening a combinatorial peptide library presented in the
 CC form of cells which coexpress the receptor or its ligand-binding receptor
 CC moiety and one member of the library, together with a signal producing
 CC system for reporting binding of the peptide to the receptor. Also
 CC included is a method for predicting the receptor-modulating activity of a
 CC compound which modulates the biological activity of a receptor comprising
 CC (a) identifying peptides which bind the receptor by the method above, (b)
 CC using a number of the peptides to predict the receptor-modulating
 CC activity of a compound by (i) providing a panel of identified peptides,
 CC where the members differ in their ability to bind to the receptor
 CC depending on reference conformations the receptor is in, where the effect
 CC of a number of reference substances known to modulate the biological
 CC activity of the receptor on the binding of each member of the panel is
 CC known and is characterised as a reference fingerprint for each reference
 CC substance, (ii) screening a test substance of unknown activity relative
 CC to the receptor to determine its effect on the binding of each member of
 CC the panel to the receptor, thereby obtaining a test fingerprint for the
 CC test substance, (iii) comparing the test fingerprint to the reference
 CC fingerprints and (iv) predicting the biological activity of the test
 CC substance based on the assumption that its biological activity will be
 CC similar to that of reference substances with similar fingerprints. The
 CC method is useful for identifying a binding peptide which binds a
 CC vertebrate, mammalian, preferably human receptor, an intracellular,
 CC nuclear, oestrogen or androgen receptor. The identified peptides which
 CC bind to the receptor are useful for predicting the receptor-modulating
 CC activity of a compound (e.g. ant/agonists). The receptor-binding library
 CC members are useful in the prediction of the ability of small organic
 CC molecules, suitable for pharmaceutical use (e.g. in the case of oestrogen
 CC receptors, for breast cancer treatment), to interact with the receptor.
 CC The analyte-binding molecules can also be used for in vivo imaging. The
 CC method has several advantages over whole animal-based assay systems in
 CC that the same technology can be applied to a variety of different
 CC receptors, the system can be used for high throughput screening and
 CC compound characterisation, and gives very distinct patterns for agonists
 CC and antagonists of receptor activity using very much less protein. The
 CC present sequence is an oestrogen receptor binding peptide from a
 CC combinatorial peptide library
 CC
 XX
 SQ Sequence 15 AA;
 Query Match 39.2%; Score 29; DB 5; Length 15;
 Best Local Similarity 46.2%; Pred. No. 3.3e+02;
 Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 Oy 3 NVLIQTDOQATTR 15
 Db 3 NLCLCLDOEACSR 15
 RESULT 11
 ADM79070
 ID ADM79070 standard; peptide; 15 AA.
 XX
 AC ADM79070;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Oestrogen receptor beta binding peptide #57.
 XX
 KM binding peptide; drug identification; in vivo imaging;
 KM oestrogen receptor beta.
 XX
 OS Unidentified.
 OS
 XX

PN US2003224390-A1.
 XX 04-DEC-2003.
 PD
 XX
 XX
 PF 17-JAN-2003; 2003US-00346162.
 XX
 PR 12-JUL-2000; 2000US-00614865.
 PR 21-MAY-2001; 2001US-00860688.
 PR 11-JUL-2001; 2001WO-US021867.
 XX
 PA (KARO-) KARO BIO AB.
 XX
 PI Fowlkes DM, Barnett TR, Buehrer B;
 XX WPI; 2004-060539/06.
 DR
 XX
 PT Identifying a binding peptide that binds a receptor, for use as a
 PT therapeutic or diagnostic agent, comprises screening a combinatorial
 PT peptide library presented in cells co-expressing a peptide, a receptor
 PT and a signal producing system.
 XX
 XX Example; SEQ ID NO 192; 66pp; English.
 PS
 CC The invention relates to a method of identifying a binding peptide which
 CC binds a receptor comprising screening a combinatorial peptide library
 CC presented in cells which co-expresses one member peptide and the
 CC receptor, together with a signal producing system for reporting binding.
 CC The method is useful in identifying drugs which can mediate the
 CC biological activity of a target protein. The receptor-binding library
 CC members may be used as therapeutic or diagnostic reagents, for in vivo
 CC imaging, or to purify target from a fluid, e.g. blood. The present
 CC sequence represents an oestrogen receptor beta binding peptide.
 CC
 XX Sequence 15 AA:
 SQ

Query Match 39.2%; Score 29; DB 8; Length 15;
 Best Local Similarity 46.2%; Pred. No. 3.3e+02;
 Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 NVLIQTDOQATTR 15
 ||| ||:| |||
 Db 3 NLTCLLDQDACS 15

RESULT 12
 ADR10604
 ID ADR10604 standard; peptide; 15 AA.
 XX
 AC ADR10604;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Sheep IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 4.
 XX
 KW Antiaesthetic; Antiallergic; Immunosuppressive; IGE; dog; asthma;
 KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
 KW sheep.
 XX
 OS Ovis aries.
 OS
 PN WO2004065936-A2.
 XX
 PD 05-AUG-2004.
 PD
 PF 15-JAN-2004; 2004WO-US003566.
 PF
 PR 16-JAN-2003; 2003US-0440472P.
 PR
 PA (UTNC-) UNIV NORTH CAROLINA STATE.
 PA
 PI Hammerberg B;
 XX
 XX WPI; 2004-593545/57.
 DR

XX Novel antibody that specifically binds to mammalian IGE epitope, useful
 PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE
 PT or treating asthma or anaphylactic shock.
 PT
 XX
 XX Example 6; Page 9; 14pp; English.
 PS

CC The present invention relates to a novel monoclonal antibody (1) that
 CC specifically binds to a mammalian IGE epitope, where the epitope is
 CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
 CC (1) is useful for testing an allergen reactivity of an IGE sample. The
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
 CC and corn allergens. The sample is a biological sample collected from a
 CC dog, cat or horse. (1) is also useful for detecting mammalian IGE and for
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
 CC antibodies recognise epitopes on canine IGE corresponding to amino acid
 CC residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the
 CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with
 CC either pig or human epsilon-chains of IGE. The present sequence is the
 CC sheep IGE 5.91 recognition site.
 CC
 XX Sequence 15 AA:
 SQ

Query Match 39.2%; Score 29; DB 8; Length 15;
 Best Local Similarity 40.0%; Pred. No. 3.3e+02;
 Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 RNNVLIQTDOQATTR 15
 ||| ||:| |||
 Db 1 RNKELMRGQHHTTQ 15

RESULT 13
 AEC98485
 ID AEC98485 standard; peptide; 15 AA.
 XX
 AC AEC98485;
 XX
 DT 01-DEC-2005 (first entry)
 XX
 DE HLA-DR binding epitope from HPV E1 protein #185.
 XX
 KW Human papilloma virus infection; virucide; cancer; cytostatic; vaccine;
 KW epitope mapping; immune stimulation; cytotoxic T-lymphocyte;
 KW human leukocyte antigen.
 XX
 OS Human papillomavirus.
 OS
 PN WO2005089164-A2.
 XX
 PD 29-SEP-2005.
 PD
 PF 03-JAN-2005; 2005WO-US000077.
 PF
 PR 31-DEC-2003; 2003US-0533211P.
 PR
 PR 02-JUL-2004; 2004US-0584652P.
 XX
 XX (EPTM-) EPIMUNE INC.
 PA (INNO-) INNOGENETICS NV.
 PA (CHES-) CHESNOT R.
 PA (NEWM-) NEWMAN M J.
 PA (MOTH-) MOTHER B.
 PA (BAKE-) BAKER D.
 PA (SOUT-) SOUTHWOOD S.
 PA (BABE-) BABE L M.
 PA (CHEN-) CHEN Y.
 PA (DEYO-) DEYOUNG L M.
 PA (HUAN-) HUANG M T F.
 PA (POWE-) POWER S D.
 XX

PI Chesnut R, Newman MJ, Mothe B, Baker D, Southwood S, Babe LM;
PI Chen Y, Deyoung LM, Huang MTF, Power SD;
XX WPI; 2005-658982/67.
XX
XX New polynucleotide comprises a multi-epitope construct comprising nucleic
PT acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte
PT (CTL) epitopes, useful in preparing a vaccine against HPV.
XX
XX Disclosure; Page 325; 518pp; English.
XX
XX The invention relates to a new polynucleotide comprising a multi-epitope
CC construct comprising nucleic acids encoding the human papillomavirus
CC (HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16.E1.214, and that
CC are directly or indirectly joined to one another in the same reading
CC frame, a vaccine minigene. Also included are a vector comprising the
CC multi-epitope construct, a polypeptide comprising an amino acid sequence
CC encoded by the polynucleotide, a composition (comprising the
CC polynucleotide, vector and/or polypeptide and a carrier), a cell
CC (comprising the polynucleotide, vector or polypeptide), inducing an
CC immune response against human papillomavirus virus (HPV) and making the
CC polynucleotide, vector or polypeptide. The epitopes are derived from
CC different strains of HPV and are from the E1, E2, E6 and E7 proteins. The
CC epitopes may be linked via a GP-anchor/spacer peptide. The order of the
CC epitopes in the vaccine protein are disclosed in the tables referred to
CC in the claims of the specification. The polynucleotide, vector or
CC polypeptide is useful in preparing a composition for inducing an immune
CC response against human papillomavirus virus (HPV) and thus providing a
CC defense against HPV infection and HPV-related cancers. The present
CC sequence is an HPV-derived peptide and HPV-related cancers. The present
CC human leukocyte antigen (HLA) peptides.
XX
SQ Sequence 15 AA;
Query Match 37.8%; Score 28; DB 9; Length 15;
Best Local Similarity 40.0%; Pred. No. 5e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
OY 5 LIQTDQQAATT 14
Db 3 MVQVEEQQT 12
RESULT 14
AEC98272
ID AEC98272 standard; peptide; 15 AA.
XX
AC AEC98272;
XX
DT 01-DEC-2005 (first entry)
XX
DE HLA-DR binding epitope from HPV E1 protein #40.
XX
XX Human papilloma virus infection; virucide; cancer; cytostatic; vaccine;
KM epitope mapping; immune stimulation; cytotoxic T-lymphocyte;
KM human leukocyte antigen.
XX
OS Human papillomavirus.
XX
PN WO2005089164-A2.
XX
PD 29-SEP-2005.
XX
PF 03-JAN-2005; 2005WO-US000077.
XX
XX 31-DEC-2003; 2003US-053211P.
PR 02-JUL-2004; 2004US-0584652P.
XX
PA (EPIM-) EPIMUNE INC.
PA (INNO-) INNOGENETICS NV.
PA (CHES/) CHESNUT R.
PA (NEWM/) NEWMAN M J.
PA (MOTH/) MOTHE B.

PA (BAKE/) BAKER D.
PA (SOUT/) SOUTHWOOD S.
PA (BABE/) BABE L M.
PA (CHEN/) CHEN Y.
PA (DEYO/) DEYOUNG L M.
PA (HUAN/) HUANG M T F.
PA (POWE/) POWER S D.
XX
PI Chesnut R, Newman MJ, Mothe B, Baker D, Southwood S, Babe LM;
PI Chen Y, Deyoung LM, Huang MTF, Power SD;
XX WPI; 2005-658982/67.
XX
XX New polynucleotide comprises a multi-epitope construct comprising nucleic
PT acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte
PT (CTL) epitopes, useful in preparing a vaccine against HPV.
XX
XX Disclosure; Page 315; 518pp; English.
XX
XX The invention relates to a new polynucleotide comprising a multi-epitope
CC construct comprising nucleic acids encoding the human papillomavirus
CC (HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16.E1.214, and that
CC are directly or indirectly joined to one another in the same reading
CC frame, a vaccine minigene. Also included are a vector comprising the
CC multi-epitope construct, a polypeptide comprising an amino acid sequence
CC encoded by the polynucleotide, a composition (comprising the
CC polynucleotide, vector and/or polypeptide and a carrier), a cell
CC (comprising the polynucleotide, vector or polypeptide), inducing an
CC immune response against human papillomavirus virus (HPV) and making the
CC polynucleotide, vector or polypeptide. The epitopes are derived from
CC different strains of HPV and are from the E1, E2, E6 and E7 proteins. The
CC epitopes may be linked via a GP-anchor/spacer peptide. The order of the
CC epitopes in the vaccine protein are disclosed in the tables referred to
CC in the claims of the specification. The polynucleotide, vector or
CC polypeptide is useful in preparing a composition for inducing an immune
CC response against human papillomavirus virus (HPV) and thus providing a
CC defense against HPV infection and HPV-related cancers. The present
CC sequence is an HPV-derived peptide and HPV-related cancers. The present
CC human leukocyte antigen (HLA) peptides.
XX
SQ Sequence 15 AA;
Query Match 37.8%; Score 28; DB 9; Length 15;
Best Local Similarity 40.0%; Pred. No. 5e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
OY 5 LIQTDQQAATT 14
Db 1 MVQVEEQQT 10
RESULT 15
AAG95534
ID AAG95534 standard; peptide; 10 AA.
XX
AC AAG95534;
XX
DT 18-SEP-2001 (first entry)
XX
DE Human complementary peptide, SEQ ID NO: 1728.
XX
XX Human; complementary peptide; ligand; drug discovery; drug design.
XX
OS Homo sapiens.
XX
PN WO200142277-A2.
XX
PD 14-JUN-2001.
XX
XX 13-DEC-2000; 2000WO-GB004776.
PR 13-DEC-1999; 99GB-00029464.
XX

PA (PROT-) PROTEOM LTD.
 XX
 PI Roberts GW, Heal JR,
 XX
 DR WPI; 2001-408419/43.

XX A set of peptide ligands consisting of specific complementary peptides to
 PT proteins encoded by genes of the human genome, useful in an assay for
 PT screening and identifying of one or more novel peptides which are drug
 PT candidates or pro-drugs.

XX
 PS Example 4; Page 290; 646pp; English.

CC The invention relates to a set of complementary peptide ligands generated
 CC from the human genome. The complementary peptides interact with their
 CC relevant target proteins encoded in the human genome. They can be used as
 CC reagents in drug discovery and as lead ligands to facilitate drug design
 CC and development. The present sequence is a complementary peptide provided
 CC in the specification

XX
 SQ Sequence 10 AA;

Query Match 36.5%; Score 27; DB 4; Length 10;
 Best Local Similarity 71.4%; Pred. No. 4.9e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 8 TDQQT 14
 :|||
 Db 1 SDQQT 7 ;

Search completed: May 30, 2006, 10:12:42
 Job time : 62 secs

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OM protein - protein search, using sw model

Run on: May 30, 2006, 10:21:55 ; Search time 47 Seconds

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147.835 Million cell updates/sec

Title: US-10-758-165A-3

Sequence: 1 RNNVLIQTDOQATTR 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqe, 463214858 residues

Total number of hits satisfying chosen parameters: 395127

Minimum DB seq length: 0
Maximum DB seq length: 15Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:*

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- 2: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US09_PUBCOMB.pep:*
- 4: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US10A_PUBCOMB.pep:*
- 5: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US10B_PUBCOMB.pep:*
- 6: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	100.0	15	5	US-10-758-165-3
2	49	66.2	15	4	US-10-052-788-4
3	41	55.4	15	5	US-10-758-165-1
4	40	54.1	15	5	US-10-758-165-7
5	37	50.0	15	5	US-10-758-165-2
6	32	43.2	15	5	US-10-497-091-128
7	29	39.2	12	5	US-10-958-216-713
8	29	39.2	15	4	US-10-346-162-192
9	29	39.2	15	5	US-10-758-165-4
10	27	36.5	10	3	US-09-572-404B-1728
11	27	36.5	13	5	US-10-497-091-14
12	27	36.5	14	4	US-10-172-425B-37
13	27	36.5	15	5	US-10-497-091-129
14	26	35.1	12	5	US-10-935-642-48
15	26	35.1	12	6	US-11-074-477-48
16	26	35.1	13	5	US-10-497-091-15
17	25	33.8	12	3	US-09-764-868-1443
18	25	33.8	12	3	US-09-955-999-123
19	25	33.8	14	4	US-10-221-125-1
20	25	33.8	15	4	US-10-014-340-796
21	25	33.8	15	6	US-10-225-567A-1123
22	25	33.8	15	6	US-11-004-270-94
23	25	33.8	15	6	US-11-004-273-94
24	24	32.4	9	4	US-10-117-937-560
25	24	32.4	9	5	US-10-895-064-2404
26	24	32.4	9	6	US-11-067-064-560
27	24	32.4	9	6	US-11-067-159-560

28	24	32.4	9	6	US-11-129-741-2404	Sequence 2404, App
29	24	32.4	10	4	US-10-117-937-561	Sequence 561, App
30	24	32.4	10	6	US-11-067-064-561	Sequence 561, App
31	24	32.4	10	6	US-11-067-159-561	Sequence 561, App
32	24	32.4	12	4	US-10-097-175-66	Sequence 66, Appl
33	24	32.4	12	4	US-10-264-109-289	Sequence 289, App
34	24	32.4	12	5	US-10-264-109-289	Sequence 289, App
35	24	32.4	13	3	US-09-791-378-584	Sequence 584, App
36	24	32.4	13	3	US-09-791-377-584	Sequence 584, App
37	24	32.4	13	4	US-10-014-340-569	Sequence 569, App
38	24	32.4	13	4	US-10-014-340-569	Sequence 569, App
39	24	32.4	13	4	US-10-014-338-7	Sequence 31, Appl
40	24	32.4	13	4	US-10-369-736-31	Sequence 31, Appl
41	24	32.4	13	4	US-10-112-582-14	Sequence 14, Appl
42	24	32.4	13	4	US-10-369-738-31	Sequence 31, Appl
43	24	32.4	13	5	US-10-808-187-706	Sequence 706, App
44	24	32.4	13	5	US-10-807-807-706	Sequence 706, App
45	24	32.4	13	6	US-11-028-058-31	Sequence 31, Appl

ALIGNMENTS

```
RESULT 1
US-10-758-165-3
; Sequence 3, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hamnerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758.165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Equus caballus
US-10-758-165-3

Query Match      100.0%; Score 74; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. NO. 2.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RNNVLIQTDOQATTR 15
DB      1 RNNVLIQTDOQATTR 15

RESULT 2
US-10-052-788-4
; Sequence 4, Application US/10052788
; Publication No. US20030087314A1
; GENERAL INFORMATION:
; APPLICANT: Gershwin, Laurel J.
; APPLICANT: Pettigrew, Howard David
; APPLICANT: Kalina, Warren V.
; TITLE OF INVENTION: Epsilon Immunoglobulin Chain Derived Peptides for
; FILE REFERENCE: 023070-121000US
; CURRENT APPLICATION NUMBER: US/10/052.788
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

OTHER INFORMATION: Description of Artificial Sequence:epitope peptide
OTHER INFORMATION: P4, early portion of C4 of equine IgE epsilon
OTHER INFORMATION: heavy chain
US-10-052-788-4

Query Match 66.2%; Score 49; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.078;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 IOTDQOATTR 15
|:|:|:|:|:|:|
DB 1 IOTDQOATTR 10

RESULT 3
US-10-758-165-1

Sequence 1, Application US/10758165
Publication No. US20050196816A1

GENERAL INFORMATION:

APPLICANT: Hammerberg, Bruce

TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES

FILE REFERENCE: 5051-661

CURRENT FILING DATE: 2004-01-16

PRIOR APPLICATION NUMBER: US 60/440,472

PRIOR FILING DATE: 2003-01-16

NUMBER OF SEQ ID NOS: 16

SOFTWARE: PatentIn version 3.2

SEQ ID NO 1

LENGTH: 15

TYPE: PRT

ORGANISM: Canis familiaris

US-10-758-165-1

Query Match 55.4%; Score 41; DB 5; Length 15;
Best Local Similarity 64.3%; Pred. No. 2.2;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 RNNVLIQTDOQATT 14
|:|:|:|:|:|:|
DB 1 RNDSPICDTQYTTT 14

RESULT 4
US-10-758-165-7

Sequence 7, Application US/10758165
Publication No. US20050196816A1

GENERAL INFORMATION:

APPLICANT: Hammerberg, Bruce

TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES

FILE REFERENCE: 5051-661

CURRENT APPLICATION NUMBER: US/10/758,165

CURRENT FILING DATE: 2004-01-16

PRIOR APPLICATION NUMBER: US 60/440,472

PRIOR FILING DATE: 2003-01-16

NUMBER OF SEQ ID NOS: 16

SOFTWARE: PatentIn version 3.2

SEQ ID NO 7

LENGTH: 15

TYPE: PRT

ORGANISM: Sus scrofa

US-10-758-165-7

Query Match 54.1%; Score 40; DB 5; Length 15;
Best Local Similarity 46.7%; Pred. No. 3.3;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

OY 1 RNNVLIQTDOQATTR 15
|:|:|:|:|:|:|
DB 1 RNDAPVQADRHSTTR 15

RESULT 5

US-10-758-165-2

Sequence 2, Application US/10758165

Publication No. US20050196816A1

GENERAL INFORMATION:

APPLICANT: Hammerberg, Bruce

TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES

FILE REFERENCE: 5051-661

CURRENT APPLICATION NUMBER: US/10/758,165

CURRENT FILING DATE: 2004-01-16

PRIOR APPLICATION NUMBER: US 60/440,472

PRIOR FILING DATE: 2003-01-16

NUMBER OF SEQ ID NOS: 16

SOFTWARE: PatentIn version 3.2

SEQ ID NO 2

LENGTH: 15

TYPE: PRT

ORGANISM: Felis catus

US-10-758-165-2

Query Match 50.0%; Score 37; DB 5; Length 15;
Best Local Similarity 53.8%; Pred. No. 11;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 2 NNVLITDQOATT 14
|:|:|:|:|:|:|
DB 2 NDSPVTEQOATT 14

RESULT 6
US-10-497-091-128

Sequence 128, Application US/10497091
Publication No. US20050074863A1

GENERAL INFORMATION:

APPLICANT: HELLEDOORN, Koen

APPLICANT: BAKER, Matthew

APPLICANT: WILLIAMS, Steven

APPLICANT: CARR, Francis J.

TITLE OF INVENTION: T-CELL EPITOPES IN CARBOXYPEPTIDASE G2

FILE REFERENCE: MER-130

CURRENT APPLICATION NUMBER: US/10/497,091

CURRENT FILING DATE: 2004-05-28

PRIOR APPLICATION NUMBER: PCT/EP02/13351

PRIOR FILING DATE: 2002-11-27

PRIOR APPLICATION NUMBER: EP02020634.8

PRIOR FILING DATE: 2002-09-13

PRIOR APPLICATION NUMBER: EP02001778.6

PRIOR FILING DATE: 2002-01-25

PRIOR APPLICATION NUMBER: EP01128519.4

PRIOR FILING DATE: 2001-11-29

NUMBER OF SEQ ID NOS: 312

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 128

LENGTH: 15

TYPE: PRT

ORGANISM: homo sapiens

US-10-497-091-128

Query Match 43.2%; Score 32; DB 5; Length 15;
Best Local Similarity 61.5%; Pred. No. 90;
Matches 8; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

OY 1 RNNVLIQ-TDQ 11
|:|:|:|:|:|:|
DB 3 RDNVLFQATDEQ 15

RESULT 7
US-10-958-216-713

Sequence 713, Application US/10958216
Publication No. US20050181388A1

GENERAL INFORMATION:

APPLICANT: EDWARDS, ALED

APPLICANT: DHARAMSI, AKIL

APPLICANT: VEDADI, MASOUD
APPLICANT: ALAM, MUHAMMAD ZAHOR
APPLICANT: ARROWSMITH, CHERYL
APPLICANT: AMREY, DONALD E.
APPLICANT: BEATTIE, BRYAN
APPLICANT: BUZADZKA, KRISTINA
APPLICANT: CANADIEN, VERONICA
APPLICANT: DOMAGALA, MEGAN
APPLICANT: HOUSTON, SIMON
APPLICANT: KANAGARAJAH, DHUSHY
APPLICANT: LI, QIN
APPLICANT: MANSOURY, KAMRAN
APPLICANT: McDONALD, MERRY-LYNN
APPLICANT: NETHERY, KATHLEEN
APPLICANT: NG, IVY
APPLICANT: OUYANG, HUI
APPLICANT: PINDER, BENJAMIN
APPLICANT: RICHARDS, DAWN
APPLICANT: TAI, MATTHEW
APPLICANT: THALAKADA, ROSANNE
APPLICANT: VALLEE, FRANCOIS
APPLICANT: VIRAG, CRISTINA
TITLE OF INVENTION: NOVEL PURIFIED POLYPEPTIDES FROM BACTERIA
FILE REFERENCE: IPT-205.01
CURRENT APPLICATION NUMBER: US/10/958,216
CURRENT FILING DATE: 2004-10-04
PRIOR APPLICATION NUMBER: PCT/CA03/00462
PRIOR FILING DATE: 2003-04-02
PRIOR APPLICATION NUMBER: 60/369,511
PRIOR FILING DATE: 2002-04-02
PRIOR APPLICATION NUMBER: 60/385,089
PRIOR FILING DATE: 2002-05-31
PRIOR APPLICATION NUMBER: 60/385,751
PRIOR FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: 60/386,553
PRIOR FILING DATE: 2002-06-05
PRIOR APPLICATION NUMBER: 60/386,577
PRIOR FILING DATE: 2002-06-05
PRIOR APPLICATION NUMBER: 60/386,367
PRIOR FILING DATE: 2002-06-05
PRIOR APPLICATION NUMBER: 60/386,566
PRIOR FILING DATE: 2002-06-05
PRIOR APPLICATION NUMBER: 60/386,390
PRIOR FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: 60/386,601
PRIOR FILING DATE: 2002-06-06
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1132
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 713
LENGTH: 12
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-10-958-216-713

Query Match 39.2% Score 29; DB 5; Length 12;
Best Local Similarity 33.3%; Pred. No. 2.4e+02;
Matches 4; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 4 VLIOFDOQATTR 15
DB 1 VMVGEDEASVR 12

RESULT 8
US-10-346-162-192
Sequence 192, Application US/10346162
Publication No. US20030224390A1
GENERAL INFORMATION:
APPLICANT: KARO BIO USA, INC.
APPLICANT: FOWLES, Dana M.
APPLICANT: BARNETT, Thomas R.
APPLICANT: BUHRER, Benjamin

TITLE OF INVENTION: METHOD OF IDENTIFYING CONFORMATION-SENSITIVE BINDING PEPTIDES AND
FILE REFERENCE: PAGE-1H
CURRENT APPLICATION NUMBER: US/10/346,162
CURRENT FILING DATE: 2003-01-17
PRIOR APPLICATION NUMBER: US 09/614,865
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 09/860,688
PRIOR FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 268
SOFTWARE: PatentIn version 3.1
SEQ ID NO 192
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic
US-10-346-162-192

Query Match 39.2% Score 29; DB 4; Length 15;
Best Local Similarity 46.2%; Pred. No. 3.1e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 NVLIOTDQATTR 15
DB 3 NLCLIDQACSR 15

RESULT 9
US-10-758-165-4
Sequence 4, Application US/10758165
Publication No. US20050196616A1
GENERAL INFORMATION:
APPLICANT: Hammerberg, Bruce
TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
FILE REFERENCE: 5051-661
CURRENT APPLICATION NUMBER: US/10/758,165
CURRENT FILING DATE: 2004-01-16
PRIOR APPLICATION NUMBER: US 60/440,472
PRIOR FILING DATE: 2003-01-16
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4
LENGTH: 15
TYPE: PRT
ORGANISM: Ovis aries
US-10-758-165-4

Query Match 39.2% Score 29; DB 5; Length 15;
Best Local Similarity 40.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 RNNVLIOTDQATTR 15
DB 1 RNKELMRGQHTTQ 15

RESULT 10
US-09-572-404B-1728
Sequence 1728, Application US/09572404B
Publication No. US20030078374A1
GENERAL INFORMATION:
APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome
FILE REFERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProtPatent version 1.0
SEQ ID NO 1728
LENGTH: 10
TYPE: PRT
ORGANISM: Homo Sapiens

FEATURE:
OTHER INFORMATION: sequence located in TPP2 at 1925-1934 and may interact with Sequ
OTHER INFORMATION: 1727 in this patent.
US-09-572-404B-1728

Query Match 36.5%; Score 27; DB 3; Length 10;
Best Local Similarity 71.4%; Pred. No. 4.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 TDQATT 14
:|||||
Db 1 SDQOTT 7

RESULT 11
US-10-497-091-14
Sequence 14, Application US/10497091
Publication No. US20050074863A1
GENERAL INFORMATION:
APPLICANT: HELLEDOORN, Koen
APPLICANT: BAKER, Matthew
APPLICANT: WILLIAMS, Steven
APPLICANT: CARR, Francis J.
TITLE OF INVENTION: T-CELL EPITOPES IN CARBOXYPEPTIDASE G2
FILE REFERENCE: MER-130
CURRENT APPLICATION NUMBER: US/10/497,091
CURRENT FILING DATE: 2004-05-28
PRIOR APPLICATION NUMBER: PCT/EP02/13351
PRIOR FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: EP02020634.8
PRIOR FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: EP02001778.6
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: EP01128519.4
PRIOR FILING DATE: 2001-11-29
NUMBER OF SEQ ID NOS: 312
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 13
TYPE: PRT
ORGANISM: homo sapiens
US-10-497-091-14

Query Match 36.5%; Score 27; DB 5; Length 13;
Best Local Similarity 58.3%; Pred. No. 6.1e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 2 NNVLIQ--TDQ 11
:|||||:
Db 1 DNVLFOATDEQ 12

RESULT 12
US-10-172-425B-37
Sequence 37, Application US/10172425B
Publication No. US20030147908A1
GENERAL INFORMATION:
APPLICANT: Kaempfer, Raymond
APPLICANT: Ared, Gila
TITLE OF INVENTION: BROAD SPECTRUM ANTAGONISTS AND VACCINES
FILE REFERENCE: A31967-PCT-USA-A 066031.0164
CURRENT APPLICATION NUMBER: US/10/172,425B
CURRENT FILING DATE: 2002-06-13
PRIOR APPLICATION NUMBER: 09/150,947
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: PCT/IL97/00438
PRIOR FILING DATE: 1997-12-30
PRIOR APPLICATION NUMBER: ISRAEL 119938
PRIOR FILING DATE: 1996-12-30
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 37

LENGTH: 14
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-172-425B-37

Query Match 36.5%; Score 27; DB 4; Length 14;
Best Local Similarity 44.4%; Pred. No. 6.6e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 6 IOTDQATT 14
:|||||:
Db 1 VOTDKSVT 9

RESULT 13
US-10-497-091-129
Sequence 129, Application US/10497091
Publication No. US20050074863A1
GENERAL INFORMATION:
APPLICANT: HELLEDOORN, Koen
APPLICANT: BAKER, Matthew
APPLICANT: WILLIAMS, Steven
APPLICANT: CARR, Francis J.
TITLE OF INVENTION: T-CELL EPITOPES IN CARBOXYPEPTIDASE G2
FILE REFERENCE: MER-130
CURRENT APPLICATION NUMBER: US/10/497,091
CURRENT FILING DATE: 2004-05-28
PRIOR APPLICATION NUMBER: PCT/EP02/13351
PRIOR FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: EP02020634.8
PRIOR FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: EP02001778.6
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: EP01128519.4
PRIOR FILING DATE: 2001-11-29
NUMBER OF SEQ ID NOS: 312
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 129
LENGTH: 15
TYPE: PRT
ORGANISM: homo sapiens
US-10-497-091-129

Query Match 36.5%; Score 27; DB 5; Length 15;
Best Local Similarity 58.3%; Pred. No. 7.2e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 2 NNVLIQ--TDQ 11
:|||||:
Db 1 DNVLFOATDEQ 12

RESULT 14
US-10-935-642-48
Sequence 48, Application US/10935642
Publication No. US20050050656A1
GENERAL INFORMATION:
APPLICANT: Huang, Xueying
APPLICANT: Wang, Hong
TITLE OF INVENTION: Peptide-Based Conditioners and Colorants for Hair, Skin, and
FILE REFERENCE: CL2296 US NA
CURRENT APPLICATION NUMBER: US/10/935,642
CURRENT FILING DATE: 2004-09-07
NUMBER OF SEQ ID NOS: 104
SOFTWARE: PatentIn version 3.2
SEQ ID NO 48
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Hair-binding peptide

US-10-935-642-48

Query Match 35.1%; Score 26; DB 5; Length 12;
Best Local Similarity 62.5%; Pred. No. 8.4e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 8 TDQCATR 15
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|
Db 1 TDMQAPTK 8

RESULT 15

US-11-074-473-48
; Sequence 48, Application US/11074473
; Publication No. US20050226839A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Xueying
; APPLICANT: Wang, Hong
; APPLICANT: Mu, Ying
; TITLE OF INVENTION: Peptide-Based Conditioners and Colorants for Hair, Skin, and
; TITLE OF INVENTION: Nail
; FILE REFERENCE: CL2296 US NA
; CURRENT APPLICATION NUMBER: US/11/074,473
; CURRENT FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: US/10/935,642
; PRIOR FILING DATE: 2004-09-07
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 48
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hair-binding peptide
US-11-074-473-48

Query Match 35.1%; Score 26; DB 6; Length 12;
Best Local Similarity 62.5%; Pred. No. 8.4e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 8 TDQCATR 15
|||
|
Db 1 TDMQAPTK 8

Search completed: May 30, 2006, 10:24:41
Job time : 47 secs

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 30, 2006, 10:22:25 ; Search time 5.66667 Seconds
(without alignments)
29.481 Million cell updates/sec

Title: US-10-758-165A-3
Perfect score: 74
Sequence: 1 RNNVLIOTDQQTTR 15

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Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 1113735 residues

Total number of hits satisfying chosen parameters: 10973

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New*

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4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
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8: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	35.1	10	US-10-516-079-64	Sequence 64, Appl
2	22	29.7	9	US-10-516-079-94	Sequence 94, Appl
3	22	29.7	14	US-11-118-524-5	Sequence 5, Appl
4	21	28.4	9	US-10-516-079-90	Sequence 90, Appl
5	20	27.0	11	US-10-538-066-625	Sequence 625, Appl
6	20	27.0	11	US-10-538-066-4	Sequence 4, Appl
7	20	27.0	14	US-11-176-182-52	Sequence 52, Appl
8	19	25.7	9	US-10-538-066-159	Sequence 159, Appl
9	19	25.7	9	US-10-473-691B-7	Sequence 7, Appl
10	19	25.7	10	US-11-140-487A-1987	Sequence 1987, Appl
11	19	25.7	12	US-11-176-182-112	Sequence 112, Appl
12	19	25.7	13	US-11-176-182-17	Sequence 17, Appl
13	19	25.7	13	US-11-122-986-822	Sequence 822, Appl
14	19	25.7	15	US-11-140-487A-2124	Sequence 2124, Appl
15	19	25.7	15	US-11-140-487A-2125	Sequence 2125, Appl
16	19	25.7	15	US-11-140-487A-2240	Sequence 2240, Appl
17	19	25.7	15	US-11-140-487A-2241	Sequence 2241, Appl
18	19	25.7	15	US-11-140-487A-2241	Sequence 2241, Appl
19	18	24.3	9	US-10-538-066-65	Sequence 65, Appl
20	18	24.3	9	US-10-538-066-66	Sequence 66, Appl
21	18	24.3	9	US-11-140-487A-343	Sequence 343, Appl
22	18	24.3	9	US-11-140-487A-437	Sequence 437, Appl
23	18	24.3	9	US-11-140-487A-546	Sequence 546, Appl
24	18	24.3	9	US-11-140-487A-1988	Sequence 1988, Appl
25	18	24.3	10	US-10-538-066-267	Sequence 267, Appl

26	18	24.3	10	6	US-10-538-066-268	Sequence 268, Appl
27	18	24.3	10	6	US-10-538-066-574	Sequence 574, Appl
28	18	24.3	10	7	US-11-140-487A-994	Sequence 994, Appl
29	18	24.3	10	7	US-11-140-487A-1989	Sequence 1989, Appl
30	18	24.3	11	6	US-10-538-066-479	Sequence 479, Appl
31	18	24.3	11	6	US-10-538-066-636	Sequence 636, Appl
32	18	24.3	12	7	US-11-122-986-570	Sequence 570, Appl
33	18	24.3	15	6	US-10-514-263-6	Sequence 6, Appl
34	18	24.3	15	6	US-11-122-986-725	Sequence 725, Appl
35	17	23.0	4	7	US-11-252-276-62	Sequence 62, Appl
36	17	23.0	8	7	US-11-122-986-30	Sequence 30, Appl
37	17	23.0	9	6	US-10-516-079-91	Sequence 91, Appl
38	17	23.0	9	7	US-11-122-986-263	Sequence 263, Appl
39	17	23.0	10	6	US-10-614-959-26	Sequence 26, Appl
40	17	23.0	10	6	US-10-538-066-240	Sequence 240, Appl
41	17	23.0	11	7	US-11-122-986-655	Sequence 655, Appl
42	17	23.0	13	7	US-11-298-718-44	Sequence 44, Appl
43	17	23.0	13	7	US-11-142-051-12	Sequence 12, Appl
44	17	23.0	14	7	US-11-176-182-63	Sequence 63, Appl
45	17	23.0	14	7	US-11-176-182-114	Sequence 114, Appl

ALIGNMENTS

```
RESULT 1
US-10-516-079-64
; Sequence 64, Application US/10516079
; Publication No. US20060088899A1
; GENERAL INFORMATION:
; APPLICANT: ALVAREZ, Vernon L.
; APPLICANT: GRIMES, Carol A.
; TITLE OF INVENTION: Combination chemotherapy with chlorotoxin
; FILE REFERENCE: 51530-5006-WO
; CURRENT APPLICATION NUMBER: US/10/516,079
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: US 60/406,033
; PRIOR FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: US 60/384,171
; PRIOR FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Pep21-SCX8_LEIGH sequence
US-10-516-079-64

Query Match
Best Local Similarity 35.1%; Score 26; DB 6; Length 10;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      8 TDQQTTR 15
      |||||
Db      2 TDQQTTR 9

RESULT 2
US-10-516-079-94
; Sequence 94, Application US/10516079
; Publication No. US20060088899A1
; GENERAL INFORMATION:
; APPLICANT: ALVAREZ, Vernon L.
; APPLICANT: GRIMES, Carol A.
; APPLICANT: GONDA, Matthew A.
; TITLE OF INVENTION: Combination chemotherapy with chlorotoxin
; FILE REFERENCE: 51530-5006-WO
; CURRENT APPLICATION NUMBER: US/10/516,079
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: US 60/406,033
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;; PRIOR FILING DATE: 2002-08-27
;; PRIOR APPLICATION NUMBER: US 60/384,171
;; PRIOR FILING DATE: 2002-05-31
;; NUMBER OF SEQ ID NOS: 95
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 94
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Mesobuthus tamulus sindicus
;; FEATURE:
;; OTHER INFORMATION: GenBank Accession No. F15229, small toxin
US-10-516-079-94

Query Match 29.7%; Score 22; DB 6; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.2e+04;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 8 TDQOATTR 15
||| :
Db 2 TDQOMSKK 9

RESULT 3
US-11-118-524-5
; Sequence 5, Application US/11118524
; Publication No. US20060088847A1
; GENERAL INFORMATION:
; APPLICANT: GU, WEI
; TITLE OF INVENTION: ARF-BP1 AS MEDIATOR OF P53-DEPENDENT AND INDEPENDENT TUMOR
; FILE REFERENCE: 19240-497US2
; CURRENT APPLICATION NUMBER: US/11/118,524
; PRIOR FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: 60/610,506
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 14
; TYPE: PRT
; ORGANISM: homo sapiens
US-11-118-524-5

Query Match 29.7%; Score 22; DB 7; Length 14;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 TDQQA 12
||| :
Db 2 TDQEA 6

RESULT 4
US-10-516-079-90
; Sequence 90, Application US/10516079
; Publication No. US20060088899A1
; GENERAL INFORMATION:
; APPLICANT: ALTAREZ, Vernon L.
; APPLICANT: GRIMES, Carol A.
; APPLICANT: GONDA, Matthew A.
; TITLE OF INVENTION: Combination chemotherapy with chlorotoxin
; FILE REFERENCE: 51530-5006-WO
; CURRENT APPLICATION NUMBER: US/10/516,079
; PRIOR FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: US 60/406,033
; PRIOR FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: US 60/384,171
; PRIOR FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 90
; LENGTH: 9
; TYPE: PRT

;; ORGANISM: Artificial sequence
;; FEATURE:
;; OTHER INFORMATION: Peptide 21a-A5 sequence
US-10-516-079-90

Query Match 28.4%; Score 21; DB 6; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.2e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 8 TDQOATTR 15
||| :
Db 1 TDHQARK 8

RESULT 5
US-10-538-066-625
; Sequence 625, Application US/10538066
; Publication No. US20060094649A1
; GENERAL INFORMATION:
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen
; FILE REFERENCE: 2060.015PC06
; CURRENT APPLICATION NUMBER: US/10/538,066
; PRIOR FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US 60/432,017
; NUMBER OF SEQ ID NOS: 767
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 625
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-538-066-625

Query Match 27.0%; Score 20; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.2e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NNVL 5
||| :
Db 3 NNVL 6

RESULT 6
US-10-538-066-4
; Sequence 4, Application US/10538066
; Publication No. US20060094649A1
; GENERAL INFORMATION:
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen
; FILE REFERENCE: 2060.015PC06
; CURRENT APPLICATION NUMBER: US/10/538,066
; PRIOR FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US 60/432,017
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 767
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-538-066-4

Query Match 27.0%; Score 20; DB 6; Length 11;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 NNVL 5
||| :
Db 5 NNVL 8

```
RESULT 7
US-11-176-182-52
; Sequence 52, Application US/11176182
; Publication No. US20060088549A1
; GENERAL INFORMATION:
; APPLICANT: ARNOLD, EDWARD
; TITLE OF INVENTION: PERSTANDIG ARNOLD, GAIL
; FILE REFERENCE: PA04-701-S
; CURRENT APPLICATION NUMBER: US/11/176,182
; CURRENT FILING DATE: 2005-07-07
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 52
; LENGTH: 14
; TYPE: PRT
; ORGANISM: chimeric HIV-HRV
US-11-176-182-52

Query Match      27.0%; Score 20; DB 7; Length 14;
Best Local Similarity 50.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      7 QTDQOAT 14
      :|::|
      4 ELDRWATT 11
      :|::|

RESULT 8
US-10-538-066-159
; Sequence 159, Application US/10538066
; Publication No. US20060094649A1
; GENERAL INFORMATION:
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen
; FILE REFERENCE: 2060.015PC06
; CURRENT APPLICATION NUMBER: US/10/538,066
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US 60/432,017
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 767
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 159
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-538-066-159

Query Match      25.7%; Score 19; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.2e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 QOAT 13
      :|::|
      1 QOAT 4
      :|::|

RESULT 9
US-10-473-691B-7
; Sequence 7, Application US/10473691B
; Publication No. US2006009202A1
; GENERAL INFORMATION:
; APPLICANT: Nicolette, Charles A.
; TITLE OF INVENTION: IMMUNOLOGUIN CONSTRUCT CONTAINING TUMOR SPECIFIC P53BP2 SEQUENC
; FILE REFERENCE: 02755/100K313-US1
; CURRENT APPLICATION NUMBER: US/10/473,691B
; CURRENT FILING DATE: 2003-09-29
; PRIOR APPLICATION NUMBER: PCT/US02/10224
; PRIOR FILING DATE: 2002-04-01
```

```
; PRIOR APPLICATION NUMBER: US 60/280,733
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: P52 BP2
US-10-473-691B-7

Query Match      25.7%; Score 19; DB 6; Length 9;
Best Local Similarity 28.6%; Pred. No. 5.2e+04;
Matches 2; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY      5 LIQTDQ 11
      :|::|
      2 LVETKE 8
      :|::|

RESULT 10
US-11-140-487A-1987
; Sequence 1987, Application US/11140487A
; Publication No. US20060093617A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C vi
; FILE REFERENCE: 166
; CURRENT APPLICATION NUMBER: US/11/140,487A
; CURRENT FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: EP 04012951.2
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: EP 04447239.7
; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: EP 05102441.2
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/576,310
; PRIOR FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: US 60/622,782
; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US 60/665,395
; PRIOR FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2278
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1987
; LENGTH: 10
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-11-140-487A-1987

Query Match      25.7%; Score 19; DB 7; Length 10;
Best Local Similarity 40.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      4 VLQTDQOAT 13
      :|::|
      1 VVATDALMT 10
      :|::|

RESULT 11
US-11-176-182-112
; Sequence 112, Application US/11176182
; Publication No. US20060088549A1
; GENERAL INFORMATION:
; APPLICANT: ARNOLD, EDWARD
; TITLE OF INVENTION: PERSTANDIG ARNOLD, GAIL
; FILE REFERENCE: PA04-701-S
; CURRENT APPLICATION NUMBER: US/11/176,182
; CURRENT FILING DATE: 2005-07-07
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn version 3.3
```

```
; SEQ ID NO 112
; LENGTH: 12
; TYPE: PRT
; ORGANISM: chimeric HIV-HRV
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (12)..(12)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-11-176-182-112
```

```
Query Match          25.7%; Score 19; DB 7; Length 12;
Best Local Similarity 33.3%; Pred. No. 3.5e+02;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
OY      6 IQTDOQATT 14
       :|:|:|:|
Db      2 VELDKMAST 10
```

RESULT 12

```
; Sequence 17, Application US/11176182
; Publication No. US20060088549A1
; GENERAL INFORMATION:
; APPLICANT: ARNOLD, EDWARD
; TITLE OF INVENTION: CHIMERIC HIV VACCINE
; FILE REFERENCE: PA04-701-S
; CURRENT APPLICATION NUMBER: US/11/176,182
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 17
; LENGTH: 13
; TYPE: PRT
; ORGANISM: chimeric HIV-HRV
US-11-176-182-17
```

```
Query Match          25.7%; Score 19; DB 7; Length 13;
Best Local Similarity 33.3%; Pred. No. 3.8e+02;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
OY      6 IQTDOQATT 14
       :|:|:|:|
Db      3 VELDKMAST 11
```

RESULT 13

```
; Sequence 822, Application US/11122986
; Publication No. US20060104989A1
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, ALBD
; APPLICANT: DHARAMSI, AKIL
; APPLICANT: VEDADI, MASOUD
; TITLE OF INVENTION: ESSENTIAL NOVEL BACTERIAL POLYPEPTIDES
; FILE REFERENCE: IPR-330 01
; CURRENT APPLICATION NUMBER: US/11/122,986
; CURRENT FILING DATE: 2005-05-05
; PRIOR APPLICATION NUMBER: 60/423,875
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,832
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,915
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,757
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/423,758
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 60/424,367
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,376
; PRIOR FILING DATE: 2002-11-06
```

```
; PRIOR APPLICATION NUMBER: 60/424,370
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,362
; PRIOR FILING DATE: 2002-11-06
; PRIOR APPLICATION NUMBER: 60/424,373
; PRIOR FILING DATE: 2002-11-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 844
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 822
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-11-122-986-822
```

```
Query Match          25.7%; Score 19; DB 7; Length 13;
Best Local Similarity 40.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
OY      6 IQTDOQATTR 15
       |||:|:|:|
Db      4 INTVOELTNK 13
```

RESULT 14

```
; Sequence 2124, Application US/11140487A
; Publication No. US20060093617A1
; GENERAL INFORMATION:
; APPLICANT: Immunogenetics N.V.
; TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C vi
; FILE REFERENCE: 166
; CURRENT APPLICATION NUMBER: US/11/140,487A
; CURRENT FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: EP 04012951.2
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: EP 04447239.7
; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: EP 05102441.2
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/576,310
; PRIOR FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: US 60/622,782
; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US 60/665,395
; PRIOR FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2278
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2124
; LENGTH: 15
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-11-140-487A-2124
```

```
Query Match          25.7%; Score 19; DB 7; Length 15;
Best Local Similarity 40.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
OY      4 VLIOTDOQAT 13
       ||:|:|:|
Db      3 VVVAIDALMT 12
```

RESULT 15

```
; Sequence 2125, Application US/11140487A
; Publication No. US20060093617A1
; GENERAL INFORMATION:
; APPLICANT: Immunogenetics N.V.
; TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C vi
; FILE REFERENCE: 166
; CURRENT APPLICATION NUMBER: US/11/140,487A
; CURRENT FILING DATE: 2005-05-31
```

; PRIOR APPLICATION NUMBER: EP 04012951.2
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: EP 04447239.7
; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: EP 05102441.2
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/576,310
; PRIOR FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: US 60/622,782
; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US 60/665,395
; PRIOR FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2278
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2125
; LENGTH: 15
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-11-140-487A-2125

Query Match 25.7%; Score 19; DB 7; Length 15;
Best Local Similarity 40.0%; Pred. No. 4.5e+02;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy 4 VLIOTDQAT 13
|:|:|
Db 3 VVATDALT 12

Search completed: May 30, 2006, 10:25:04
Job time : 6.66667 secs

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APPLICANT: schooner, sue
APPLICANT: fferreb-Constant
APPLICANT: Richard

APPLICANT: Rochelleau, Thomas A.
APPLICANT: Blackburn, Michael B.
APPLICANT: Hey, Timothy D.
APPLICANT: Merlo, Donald J.
APPLICANT: Orr, Gregory L.
APPLICANT: Roberts, Jean L.
APPLICANT: Strickland, James A.
APPLICANT: Guo, Lining
APPLICANT: Cliche, Todd A.
APPLICANT: Sukhaphinda, Kitiari
TITLE OF INVENTION: Insecticidal Protein Toxins From Photobhabdus
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dow Agrosciences Patent Department
STREET: 9330 Zionsville Road
CITY: Indianapolis
STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,567B
FILING DATE: 05-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/063,615
FILING DATE: 18-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/395,497
FILING DATE: 28-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/007,255
FILING DATE: 06-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/608,423
FILING DATE: 28-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/705,484
FILING DATE: 28-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.93804
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: N-terminal
US-08-851-567B-2

Query Match 33.5%; Score 28.5; DB 2; Length 12;
Best Local Similarity 53.8%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

QY 3 DSPVTEQQAATW 15
||| |
Db 3 DSP---EVSITW 12

RESULT 3
US-09-339-922A-88
Sequence 88, Application US/09339922A
Patent No. 6531580

GENERAL INFORMATION:
APPLICANT: Huse, William D.
TITLE OF INVENTION: Anti-AlphaV Beta3 Recombinant Human Antibodies, Nucleic
FILE REFERENCE: P-IX 3536
CURRENT APPLICATION NUMBER: US/09/339,922A
CURRENT FILING DATE: 1999-06-24
NUMBER OF SEQ ID NOS: 112
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 88
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Mutated
US-09-339-922A-88

Query Match 32.9%; Score 28; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 5e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 QQAATW 15
||| |
Db 1 QQSTW 6

RESULT 4
US-09-016-061-88
Sequence 88, Application US/09016061
Patent No. 6596850
GENERAL INFORMATION:
APPLICANT: Huse, William D.
APPLICANT: Glaser, Scott M.
TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
TITLE OF INVENTION: Antibodies, Nucleic Acids Encoding Same and Methods of Use
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,061
FILING DATE: 30-JAN-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/791,391
FILING DATE: 30-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2965
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-016-061-88

Query Match 32.9%; Score 28; DB 2; Length 9;

Best Local Similarity 66.7%; Pred. No. 5e+05; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 0; Indels 0;

Qy 10 QOATW 15
Db 1 QOSTW 6

RESULT 5
5223254-6
; Patent No. 5223254
; APPLICANT: PARADISO, PETER R.; HILDETH, STEPHEN W.; HU,
; BRANDA T.; MARTIN-GALLARDO, ANTONIA; ARUMUGHAM, RASAPPA
; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS VACCINES
; NUMBER OF SEQUENCES: 17
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/247, 017
; FILING DATE: 20-SEP-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 102,180
; FILING DATE: 29-SEP-1987
; SEQ ID NO: 6:
; LENGTH: 13
5223254-6

Query Match 32.9%; Score 28; DB 7; Length 13;
Best Local Similarity 40.0%; Pred. No. 1.9e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NDSPTREQ 11
Db 2 NDMPTINDOK 11

RESULT 6
US-09-641-528B-48206
; Sequence 48206, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esben
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060 0100001
; CURRENT APPLICATION NUMBER: US/09/641, 528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172, 705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48206
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-48206

Query Match 32.9%; Score 28; DB 3; Length 15;
Best Local Similarity 42.9%; Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 HNSPVTREQAT 14
Db 2 YNSPVTNEVNT 15

RESULT 7
US-08-836-075A-166

; Sequence 166, Application US/08836075A

; Patent No. 6180768
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT
; APPLICANT: STUYVER, LIEVEN
; TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
; TITLE OF INVENTION: AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6.0 / ASCII text output
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836, 075A
; FILING DATE: 21 Apr 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/04155
; FILING DATE: 23 Oct 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94870166.9
; FILING DATE: 21 Oct 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95870076.7
; FILING DATE: 28 Jun 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: KAMMERER, PATRICIA A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: INNS:004
; INFORMATION FOR SEQ ID NO: 166:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-836-075A-166

Query Match 31.8%; Score 27; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 6 VTEQATW 15
Db 1 VRTGNSRCW 10

RESULT 8
US-09-878-281A-244
; Sequence 244, Application US/09878281A
; Patent No. 6762024
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: New sequences of hepatitis C virus genotypes for diagnosis, proph.
; FILE REFERENCE: 35
; CURRENT APPLICATION NUMBER: US/09/878, 281A
; CURRENT FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 284
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 244
; LENGTH: 13
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-09-878-281A-244

Query Match 31.8%; Score 27; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 VRTEQOATW 15
| | | | |
Db 1 VRTGNQRCW 10

RESULT 9
US-09-851-138C-166
; Sequence 166, Application US/09851138C
; Patent No. 6974864
; GENERAL INFORMATION:
; APPLICANT: INNOGENETICS N.V.
; TITLE OF INVENTION: New sequences of hepatitis C virus genotypes and their use as
; FILE REFERENCE: 2551-106
; CURRENT APPLICATION NUMBER: US/09/851,138C
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: EP 94870166.9
; PRIOR FILING DATE: 1994-10-21
; PRIOR APPLICATION NUMBER: EP 95870076.7
; PRIOR FILING DATE: 1995-06-28
; NUMBER OF SEQ ID NOS: 302
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 166
; LENGTH: 13
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-09-851-138C-166

Query Match 31.8%; Score 27; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 VRTEQOATW 15
| | | | |
Db 1 VRTGNQRCW 10

RESULT 10
US-10-000-986A-144
; Sequence 144, Application US/10000986A
; Patent No. 7005500
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephane
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: G-091US09DIV
; CURRENT APPLICATION NUMBER: US/10/000,986A
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: JPatent
; SEQ ID NO 144
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-000-986A-144

Query Match 31.8%; Score 27; DB 3; Length 14;

Best Local Similarity 33.3%; Pred. No. 3.1e+02;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 HNSPVRTEQQA 12
| | | | |
Db 2 HSDSGISVDSQS 13

RESULT 11
US-08-221-583-56
; Sequence 56, Application US/08221583
; Patent No. 5486595
; GENERAL INFORMATION:
; APPLICANT: Heaven, George A.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5486595r1e
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25:mdctchod.
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,583
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: CCOR-0185
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-221-583-56

Query Match 31.8%; Score 27; DB 1; Length 15;
Best Local Similarity 46.2%; Pred. No. 3.4e+02;
Matches 6; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 HNSPVRTEQQA 13
| | | | |
Db 1 HLPQPVSTRSQHT 13

RESULT 12
PCT-US95-04018-56
; Sequence 56, Application PC/TUS9504018
; GENERAL INFORMATION:
; APPLICANT: Heaven, George A.
; APPLICANT: Kruszyński, Marlen
; APPLICANT: Mervic, Miljenko
; APPLICANT: Weber, Robert W.
; TITLE OF INVENTION: Tumor Necrosis Factor Inhibitors
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA

ZIP: 19403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04018
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,580
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,583
FILING DATE: 01-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/221,581
FILING DATE: 01-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: CCOR-0232
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
FAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-04018-56

Query Match 31.8%; Score 27; DB 5; Length 15;
Best Local Similarity 46.2%; Pred. No. 3.4e+02;
Matches 6; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 HNDSPVTEQQT 13
Db 1 HLPQVSTRSQHT 13

RESULT 13
US-09-641-528B-4922
Sequence 4922, Application US/09641528B
Patent No. 7026443
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Cells, Esteban
APPLICANT: Grey, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 51505
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4922
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-4922

Query Match 30.6%; Score 26; DB 3; Length 9;
Best Local Similarity 55.6%; Pred. No. 5e+05;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 6 VRIEQATT 14
Db 1 VQVEEQQT 9

RESULT 14
US-09-641-528B-13784
Sequence 13784, Application US/09641528B
Patent No. 7026443
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Cells, Esteban
APPLICANT: Grey, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 51505
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13784
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-13784

Query Match 30.6%; Score 26; DB 3; Length 9;
Best Local Similarity 57.1%; Pred. No. 5e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 9 EQQATTW 15
Db 3 EQVSTW 9

RESULT 15
US-09-641-528B-26852
Sequence 26852, Application US/09641528B
Patent No. 7026443
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Cells, Esteban
APPLICANT: Grey, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 51505
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 26852
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-26852

Query Match 30.6%; Score 26; DB 3; Length 9;

Best Local Similarity 57.1%; Pred. No. 5e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 9 EQAATW 15
| : |
| : |
Db 1 EQVSTW 7

Search completed: May 30, 2006, 11:11:06
Job time : 23.333 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 30, 2006, 09:58:55 ; Search time 11.6667 Seconds
(without alignments)
123.707 Million cell updates/sec

Title: US-10-758-165A-2
Perfect score: 85
Sequence: 1 HNDSPVTEQQAATTW 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	27.1	11	2	S71304 amine oxidase (cop
2	22	25.9	15	2	PA0062 fumarate hydratase
3	21	24.7	12	2	I41235 glutamine-tryptophan
4	21	24.7	13	2	PH0138 T-cell receptor be
5	20	23.5	11	2	I52980 glucocerebrosidase
6	20	23.5	11	2	S39012 pectinase - Therm
7	20	23.5	15	2	B60763 endo-1,3-beta-gluc
8	19	22.4	9	2	A61357 phytylcaerulein -
9	19	22.4	10	2	A61337 caerulein - frog (
10	19	22.4	11	2	A29806 acidic proline-ric
11	19	22.4	11	2	A49037 TCR gamma V-J regi
12	19	22.4	12	2	E58502 43.2K bile stene p
13	19	22.4	13	2	A60458 protocatechuate 3,
14	19	22.4	13	2	S36887 ribosomal protein
15	19	22.4	14	2	S74128 superoxide dismuta
16	19	22.4	14	2	PM0147 omega-glialdin 1 a
17	19	22.4	15	2	JN0263 antigen (clone PVI
18	19	22.4	15	2	A16527 juvenile-hormone e
19	18	21.2	6	2	S78764 ribosomal protein
20	18	21.2	11	2	JQ2317 hypothetical 1.5K
21	18	21.2	12	2	PD0021 mucovate cycloisom
22	18	21.2	12	2	C30503 Ig gamma-2b chain
23	18	21.2	13	2	S33273 85K glycoprotein -
24	18	21.2	13	2	S47376 T-cell antigen rec
25	18	21.2	14	2	PH1625 Ig H chain V-D-U r
26	18	21.2	14	2	PH1627 Ig H chain V-D-U r
27	18	21.2	15	2	P00195 Sfil1-glycoprotein
28	18	21.2	15	2	S32677 nitrogene cofact
29	18	21.2	15	2	PA0020 protein QA100028 -

30	18	21.2	15	2	PA0058	protein QF200022 -
31	18	21.2	15	2	A49177	22K protein p1, mi
32	18	21.2	15	2	A53594	calnexin - mouse (
33	17	20.0	5	2	PT0580	T-cell receptor be
34	17	20.0	6	2	A31263	dehydrofolate redu
35	17	20.0	7	2	S33246	neuromodulatory pe
36	17	20.0	8	2	PT0030	inulinase (EC 3.2.
37	17	20.0	8	2	I57018	gene Cfr protein
38	17	20.0	9	2	PT0247	Ig heavy chain CRD
39	17	20.0	10	2	S66248	processing enzyme,
40	17	20.0	10	2	A60722	cryptic fibrillar p
41	17	20.0	10	2	S39030	lysoyl-bradykinin -
42	17	20.0	11	2	H54346	pyruvate synthase
43	17	20.0	11	2	B49037	TCR gamma V-J regi
44	17	20.0	11	2	C49037	TCR gamma V-J regi
45	17	20.0	11	2	A61512	variant surface gl

ALIGNMENTS

RESULT 1
S71304
amine oxidase (copper-containing) (EC 1.4.3.6) II - Aspergillus niger (fragment)
C:Species: Aspergillus niger
C>Date: 12-Feb-1998 #sequence_revision 01-May-1998 #text_change 09-Jul-2004
C:Accession: S71304
R:Frederic, I.; Tamaki, H.; Ishida, H.; Pec, P.; Luhova, L.; Tsuno, H.; Hata, M.; Asano
Eur. J. Biochem. 237, 255-265, 1996
A:Title: Two distinct quinoprotein amine oxidases are induced by n-butylamine in the myc
A:Reference number: S71303; MUID:96203933; PMID:8620882
A:Accession: S71304
A:Molecule type: protein
A:Residues: 1-11 <FRE>
A:Cross-references: UNIPROT:Q7M504; UNIPARC:UPI000017B3B7
C:Keywords: copper binding; monomer; oxidoreductase; quinoprotein; topaquione

Query Match 27.1%; Score 23; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 NDSP 5
DB 1 NDSP 4

RESULT 2
PA0062
fumarate hydratase (EC 4.2.1.2) - fungus (Fusarium sporotrichioides) (fragment)
C:Species: Fusarium sporotrichioides
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: PA0062
R:Chow, L.P.; Fukaya, N.; Sugitara, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JPIB, October 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrich
A:Reference number: PA0051
A:Accession: PA0062
A:Molecule type: protein
A:Residues: 1-15 <CHO>
A:Cross-references: UNIPROT:Q7M423; UNIPARC:UPI000017B3FD
C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 25.9%; Score 22; DB 2; Length 15;
Best Local Similarity 55.6%; Pred. No. 1.4e+03;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 4 SPVTEQQA 12
DB 1 SQRTIESDA 9

RESULT 3
I41235

glutamine-tRNA ligase (EC 6.1.1.18) - *Escherichia coli* (fragment)
C/Species: *Escherichia coli*
C/Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 03-Jun-2002
C/Accession: 141235
R/Hoben, P.; Uemura, H.; Yamao, F.; Cheung, A.; Swanson, R.; Sumner-Smith, M.; Soli, D.
Fed. Proc. 43, 2972-2976, 1984
A/Title: Misamincacylation by glutamyl-tRNA synthetase: relaxed specificity in wild-type
A/Reference number: 141235; MUID:85051900; PMID:6389180
A/Accession: 141235
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-12 <RES>
A/Cross-references: UNIPARC:UPI000016F1B4; GB:M16470; NID:G146170; PIDN:AAA69006.1; PID:
C/Keywords: aminocyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 24.7%; Score 21; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 11 QATTW 15
Db 3 EATW 7

RESULT 4
PH0138
T-cell receptor beta chain V-D-J region C8 - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 30-May-1997
C/Accession: PH0138
R/Martin, R.; Howell, M.D.; Jaraquemada, D.; Flerlage, M.; Richey, J.; Brostoff, S.; Le
J. Exp. Med. 173, 19-24, 1991
A/Title: A myelin basic protein peptide is recognized by cytotoxic T cells in the context
A/Reference number: PH0135; MUID:91086843; PMID:1702137
A/Accession: PH0138
A/Molecule type: mRNA
A/Residues: 1-13 <MAR>
A/Cross-references: UNIPARC:UPI000017C3AC
C/Keywords: T-cell receptor

Query Match 24.7%; Score 21; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 ATTW 15
Db 4 ASTM 7

RESULT 5
152980
glucocerebrosidase - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C/Accession: 152980; 165971
R/Reiner, O.; Wiggerson, M.; Horowitz, M.
DNA 7, 107-116, 1988
A/Title: Structural analysis of the human glucocerebrosidase genes.
A/Reference number: 152980; MUID:88195776; PMID:3358914
A/Accession: 152980
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-11 <RES>
A/Cross-references: UNIPARC:UPI000016A981; GB:M18916; NID:G183023; PIDN:AAA35878.1; PID:
A/Accession: 165971
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-11 <RES>
A/Cross-references: UNIPARC:UPI000016A981; GB:M18917; NID:G183025; PIDN:AAA35879.1; PID:

Query Match 23.5%; Score 20; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 SPVR 7
Db 5 SPVR 8

RESULT 6
S39012
proteinase - *Thermus* sp.
C/Species: *Thermus* sp.
C/Date: 18-Feb-1994 #sequence_revision 19-Apr-1996 #text_change 07-May-1999
C/Accession: S39012
R/Freeman, S.A.; Peek, K.; Prescott, M.; Daniel, R.
Biochem. J. 295, 463-469, 1993
A/Title: Characterization of a chelator-resistant proteinase from *Thermus* strain Rt4A2.
A/Reference number: S39012; MUID:94058984; PMID:8240244
A/Accession: S39012
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-15 <FRE>
A/Cross-references: UNIPARC:UPI00000BBFF9
A/Note: 13-Ala was also found

Query Match 23.5%; Score 20; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 10 QOATTW 15
Db 3 OSPVTW 8

RESULT 7
B60763
endo-1,3-beta-glucanase (EC 3.2.1.-), 40k - *Bacillus circulans* (strain WL-12) (fragment)
C/Species: *Bacillus circulans*
C/Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
C/Accession: B60763
R/Fiske, M.J.; Tobey-Fincher, K.L.; Fuchs, R.L.
J. Gen. Microbiol. 136, 2377-2383, 1990
A/Title: Cloning of two genes from *Bacillus circulans* WL-12 which encode 1,3-beta-glucanase
A/Reference number: A60763; MUID:91178514; PMID:2127800
A/Accession: B60763
A/Molecule type: protein
A/Residues: 1-15 <FIS>
A/Cross-references: UNIPROT:Q7ML10; UNIPARC:UPI000017AC94
C/Comment: This bacillus produces up to six different 1,3-beta-glucanases for growth on C
C/Keywords: glycosidase; hydrolase

Query Match 23.5%; Score 20; DB 2; Length 15;
Best Local Similarity 75.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 ATTW 15
Db 1 ATWW 4

RESULT 8
A61357
phyllotaerleuin - *Sauvage's* leaf frog
C/Species: *Phyllomedusa sauvagei* (*Sauvage's* leaf frog)
C/Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C/Accession: A61357
R/Manzari, A.; Bertaccini, G.; Cai, J.M.; De Caro, G.; Erspamer, V.; Impicciatore, M.
Br. J. Pharmacol. 37, 198-206, 1969
A/Title: Structure and pharmacological actions of phyllotaerleuin, a caerulein-like nona
A/Reference number: A61357; MUID:70005484; PMID:5824931
A/Accession: A61357
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-9 <ANA>
A/Cross-references: UNIPROT:Q7LZC4; UNIPARC:UPI000017668D

C:Superfamily: gastrin
C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid; skin; sulfoprotein
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:3/Binding site: sulfate (Tyr) (covalent) #status experimental
F:9/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 22.4%; Score 19; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 QOATW 15
: : :
1 QDYTCW 6

Db

RESULT 9
A61337
caerulein - frog (Hyla caerulea)
C:Species: Hyla caerulea
C>Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 07-May-1999
C:Accession: A61337
R:Anastasi, A.; Expamer, V.; Endean, R.
Arch. Biochem. Biophys. 125, 57-68, 1968
A:Title: Isolation and amino acid sequence of caerulein, the active decapeptide of the S
A:Reference number: A61337; MUID:68238534; PMID:5649531
A:Accession: A61337
A:Molecule type: protein
A:Residues: 1-10 <ANA>
A:Cross-references: UNIPARC:UPI0000126PDC
C:Comment: The last five amino acids and the carboxyl terminal amide group of this neuro
C:Superfamily: gastrin
C:Keywords: amidated carboxyl end; antihypertensive; neuropeptide; pyroglutamic acid; se
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:4/Binding site: sulfate (Tyr) (covalent) #status experimental
F:10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 22.4%; Score 19; DB 2; Length 10;
Best Local Similarity 42.9%; Pred. No. 3.1e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 9 EQOATW 15
: : :
1 QOYTCW 7

Db

RESULT 10
A29806
acidic proline-rich protein HP43b - golden hamster (fragment)
C:Species: Mesocricetus auratus (golden hamster)
C>Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 18-Jun-1993
C:Accession: A29806
R:Mahamho, H.; Ann, D.K.; Butler, L.G.; Rogler, J.; Carlson, D.M.
J. Biol. Chem. 262, 12344-12350, 1987
A:Title: Induction of proline-rich proteins in hamster salivary glands by isoproterenol
A:Reference number: A92611; MUID:87308247; PMID:3040740
A:Accession: A29806
A:Molecule type: protein
A:Residues: 1-11 <MEH>
A:Cross-references: UNIPARC:UPI000017C60F

Query Match 22.4%; Score 19; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HNDSP 5
: : :
4 YEDSP 8

Db

RESULT 11
A49037
TCR gamma V-J region - mouse (fragment)

C:Species: Mus musculus (house mouse)
C>Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: A49037
R:Esquerre, A.; Wilde, D.B.; McConnell, T.J.; Sturmhofel, K.; Valas, R.B.; Shevach, E.M.
Eur. J. Immunol. 22, 491-498, 1992
A:Title: Mouse autoreactive gamma/delta T cells. II. Molecular characterization of the T
A:Reference number: A49037; MUID:92164730; PMID:1311262
A:Accession: A49037
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-11 <EQZ>
A:Cross-references: UNIPARC:UPI00001154FA; GB:S90637; NID:G246288; PIDN:AB21547.1; PID:S
A:Experimental source: dendritic epidermal T-cell lines
A>Note: sequence extracted from NCBI backbone (NCBIN:90637, NCBI:90641)

Query Match 22.4%; Score 19; DB 2; Length 11;
Best Local Similarity 40.0%; Pred. No. 3.4e+03;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 11 QATW 15
: : :
6 RSTW 10

Db

RESULT 12
B58502
43.2K bile stone protein - unidentified bacterium (fragment)
C:Species: unidentified bacterium
C>Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 09-Jul-2004
C:Accession: B58502
R:Binette, J.P.; Binette, M.B.
submitted to the Protein Sequence Database, October 1996
A:Description: The proteins of kidney and gallbladder stones.
A:Reference number: A58501
A:Accession: B58502
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-12 <BIN>
A:Cross-references: UNIPROT:Q7M1D0; UNIPARC:UPI000017A8D4
A:Experimental source: human bile with stones
A>Note: a secondary sequence DVKIGVAGS was also found

Query Match 22.4%; Score 19; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 3.8e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 NDSPV 6
: : :
6 NEQPV 10

Db

RESULT 13
A60458
proteocatechuate 3,4-dioxygenase (EC 1.13.11.3) alpha chain - Moraxella sp. (strain GU2)
N:Alternate names: proteocatechuate oxygenase
C:Species: Moraxella sp.
C>Date: 20-Feb-1993 #sequence_revision 20-Feb-1993 #text_change 07-May-1999
C:Accession: A60458
R:Sterliades, R.; Belmont, J.
Appl. Environ. Microbiol. 55, 340-347, 1989
A:Title: Occurrence of two different forms of proteocatechuate 3,4-dioxygenase in a Morax
A:Reference number: A60458; MUID:89245845; PMID:2541659
A:Accession: A60458
A:Molecule type: protein
A:Residues: 1-13 <STB>
A:Cross-references: UNIPARC:UPI000017A9FE
A>Note: two forms P and G of the alpha subunit yielded identical amino terminal sequences
C:Keywords: iron; oxidoreductase

Query Match 22.4%; Score 19; DB 2; Length 13;
Best Local Similarity 44.4%; Pred. No. 4.1e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 7 RTEOQATW 15
 ||:|
 Db 3 RTAKRPPTY 11

RESULT 14

S36887
 ribosomal protein S14 - Mycobacterium bovis (fragments)
 C/Species: Mycobacterium bovis
 C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995
 C/Accession: S36887
 R/Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.
 FEBS Lett. 331, 9-14, 1993
 A/Title: Isolation and amino acid sequence of the 30S ribosomal protein S19 from Mycobac
 A/Reference number: S36887; MUID:94009553; PMID:8405418
 A/Accession: S36887
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-2/3-12/13 <OH>
 A/Cross-references: UNIPARC:UPI000061DAD; UNIPARC:UPI000011EC65; UNIPARC:UPI000017AD47
 C/Keywords: protein biosynthesis; ribosome

Query Match 22.4%; Score 19; DB 2; Length 13;
 Best Local Similarity 37.5%; Pred. No. 4.1e+03;
 Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 6 RTEOQAT 13
 |::||
 Db 6 VKNGRRAT 13

RESULT 15

S74128
 superoxide dismutase (EC 1.15.1.1) 1 (Ni) - Streptomyces coelicolor (fragment)
 C/Species: Streptomyces coelicolor
 C/Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 07-May-1999
 C/Accession: S74128
 R/Kim, E.J.; Kim, H.P.; Hah, Y.C.; Roe, J.H.
 Eur. J. Biochem. 241, 178-185, 1996
 A/Title: Differential expression of superoxide dismutases containing Ni and Fe/Zn in Str
 A/Reference number: S74128; MUID:97054607; PMID:8898904
 A/Accession: S74128
 A/Molecule type: protein
 A/Residues: 1-14 <KIM>
 A/Cross-references: UNIPARC:UPI000017AE10
 A/Experimental source: ATCC 10147
 C/Function:
 A/Description: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
 C/Keywords: metalloprotein; nickel; oxidoreductase; tetramer

Query Match 22.4%; Score 19; DB 2; Length 14;
 Best Local Similarity 60.0%; Pred. No. 4.5e+03;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 HNDSP 5
 |||
 Db 1 HGDLF 5

Search completed: May 30, 2006, 10:13:20
 Job time : 13 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 30, 2006, 09:59:07 ; Search time 67.3333 Seconds
(without alignments)
206.068 Million cell updates/sec

Title: US-10-758-165A-2
Perfect score: 85
Sequence: 1 HNDSPVTEQOATTW 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues
Total number of hits satisfying chosen parameters: 8966

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 7.2:*
1: uniprot_sprot:*
2: uniprot_tramb1:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	24	28.2	09F9H5_HELPY	Q9F9H5 helicobacte
2	24	28.2	06LBD0_MOUSE	Q6LBD0 mus musculu
3	23	27.1	Q7M504_ASPNG	Q7M504 aspergillus
4	22	25.9	Q47602_ECOLI	Q47602 escherichia
5	22	25.9	Q50117_MYCLE	Q50117 mycobacteri
6	22	25.9	Q7M423_FUSSP	Q7M423 fusarium sp
7	21.5	25.3	Q9T839_PPRIM	Q9T839 gorilla gor
8	21	24.7	Q9P06_FHAVU	Q9P06 phaseolus v
9	21	24.7	Q798K5_STRLI	Q798K5 streptomyce
10	21	24.7	Q9635_CHLTR	Q9635 chlamydia t
11	21	24.7	Q4A3D9_OENOE	Q4A3D9 enococcu
12	21	24.7	Q5EDJ3_LEGNP	Q5EDJ3 legionella
13	21	24.7	EP65_HUMAN	EP65 homo sapien
14	21	24.7	Q9SB03_ORISA	Q9SB03 oryza sativ
15	21	24.7	Q71G66_SHYME	Q71G66 andrena n.
16	21	24.7	Q9LCS1_AZOVI	Q9LCS1 azotobacter
17	21	24.7	Q65CH4_GEEMI	Q65CH4 tomato leaf
18	20.5	24.1	R1PL_LUPCY	R1PL lupinus cylin
19	20	23.5	Q9T2W0_YEAST	Q9T2W0 saccharomyc
20	20	23.5	Q71066_PPARA	Q71066 canine diac
21	20	23.5	Q86D30_TRYCR	Q86D30 trypanosoma
22	20	23.5	Q8TDA8_HUMAN	Q8TDA8 homo sapien
23	20	23.5	Q61DGO_CANFA	Q61DGO canis fami
24	20	23.5	Q9EQV3_MOUSE	Q9EQV3 mus musculu
25	20	23.5	Q718T2_PPARA	Q718T2 newcastle d
26	20	23.5	SODN_STRGR	SODN streptomyce
27	20	23.5	Q71G66_SHYME	Q71G66 andrena eri
28	20	23.5	Q6LBN2_BACST	Q6LBN2 bacillus st
29	20	23.5	Q71G66_SHYME	Q71G66 andrena stm
30	20	23.5	Q71H38_SHYME	Q71H38 andrena aur
31	20	23.5	Q7M110_BACCI	Q7M110 bacillus ci

ALIGNMENTS

RESULT 1	Q9F9H5_HELPY	PRELIMINARY; PRT; 10 AA.	Q9F531_thermus.ch
AC	Q9F9H5_HELPY	PRELIMINARY; PRT; 10 AA.	Q9F531_thermus.ch
DT	01-MAR-2001, integrated into UniProtKB/TrEMBL.		Q9F531_thermus.ch
DT	01-MAR-2001, sequence version 1.		Q9F531_thermus.ch
DT	07-FEB-2006, entry version 9.		Q9F531_thermus.ch
DE	Glutamate racemase (fragment).		Q9F531_thermus.ch
GN	Name=glr;		Q9F531_thermus.ch
OS	Helicobacter pylori (Campylobacter pylori).		Q9F531_thermus.ch
OC	Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;		Q9F531_thermus.ch
OC	Helicobacteraceae; Helicobacter.		Q9F531_thermus.ch
OX	NCBI_TaxID=210;		Q9F531_thermus.ch
RN	[1]		Q9F531_thermus.ch
RP	NUCLEOTIDE SEQUENCE.		Q9F531_thermus.ch
RC	STRAIN=india75A;		Q9F531_thermus.ch
RX	MEDLINE=20270152; PubMed=10809702;		Q9F531_thermus.ch
RY	DOI=10.1128/JB.182.11.3210-3218.2000;		Q9F531_thermus.ch
RA	Kersulyte D., Mukhopadhyay A.K., Velapattinam B., Su W.W., Pan Z.J.,		Q9F531_thermus.ch
RA	Gao H., Alarcon T., Lopez-Brea M., Balakrishna Nair G., Chowdhury A.,		Q9F531_thermus.ch
RA	Datta S., Shirai M., Nakazawa T., Ally R., Segal I., Wong B.C.,		Q9F531_thermus.ch
RA	Iam S.K., Olfat F.O., Boren T., Engstrand L., Torres O., Schneider R.,		Q9F531_thermus.ch
RA	Thomas J.E., Czinn S., Berg D.E.;		Q9F531_thermus.ch
RT	"Differences in genotypes of Helicobacter pylori from different human		Q9F531_thermus.ch
RT	populations.";		Q9F531_thermus.ch
RL	J. Bacteriol. 182:3210-3218 (2000).		Q9F531_thermus.ch
CC	Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms		Q9F531_thermus.ch
CC	Distributed under the Creative Commons Attribution-NonCommercial		Q9F531_thermus.ch
CC	License		Q9F531_thermus.ch
CC	-----		Q9F531_thermus.ch
DR	EMBL; AF190663; AAG18486.1; -; Genomic DNA.		Q9F531_thermus.ch
FT	NON_TER		Q9F531_thermus.ch
FT	SEQUENCE 10 AA; 1273 MW; CAD126337B133DC6 CRC64;		Q9F531_thermus.ch
SQ			Q9F531_thermus.ch
Query Match	28.2%;	Score 24; DB 2; Length 10;	
Best local Similarity	57.1%;	Pred. No. 4.1e+03;	
Matches	4; Conservative	1; Mismatches	2; Indels
		Gaps	0;
			0;
QY	9 EQOATTW 15		
DB	1 EKQKKEW 7		
RESULT 2	Q6LBD0_MOUSE	PRELIMINARY; PRT; 11 AA.	Q6LBD0_MOUSE
ID	Q6LBD0_MOUSE	PRELIMINARY; PRT; 11 AA.	Q6LBD0_MOUSE
AC	Q6LBD0_MOUSE	PRELIMINARY; PRT; 11 AA.	Q6LBD0_MOUSE
DT	05-JUL-2004, integrated into UniProtKB/TrEMBL.		Q6LBD0_MOUSE
DT	05-JUL-2004, sequence version 1.		Q6LBD0_MOUSE
DT	07-FEB-2006, entry version 8.		Q6LBD0_MOUSE
DE	Topoisomerase I (fragment).		Q6LBD0_MOUSE
GN	Name=TopI; Synonyms=TOP;		Q6LBD0_MOUSE
OS	Mus musculus (Mouse).		Q6LBD0_MOUSE

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OK NCBI_TaxID=10090;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Balb/c; TISSUE=Liver;
RX MEDLINE=94250690; PubMed=8193161;
RA Baumgartner B., Heiland S., Kunze N., Richter A., Knippers R.;
RT "Conserved regulatory elements in the type I DNA topoisomerase gene
promoters of mouse and man.";
RN Biochim. Biophys. Acta 1218:123-127(1994).
[2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Balb/c; TISSUE=Liver;
RA Baumgartner B.;
RL Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; X70958; CAA50294.1; -; Genomic_DNA.
DR MGI; MGI:98788; Top1.
DR GO; GO:0006260; P:DNA replication; IMP.
KW Isomerase.
FT NON TER 11 11
SQ SEQUENCE 11 AA; 1240 MW; 95183A9DA1E721EA CRC64;

Query Match 28.2%; Score 24; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HNSD 4
Db 7 HNSD 10

RESULT 3
ID Q7M504 ASPNG PRELIMINARY; PRT; 11 AA.
AC Q7M504;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Amine oxidase (copper-containing) (EC 1.4.3.6) II (Fragment).
OS Aspergillus niger.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OK NCBI_TaxID=5061;
RN (1)
RP PROTEIN SEQUENCE.
RX MEDLINE=96203933; PubMed=8620882;
RA Fredort J., Tamaki H., Ishida H., Pec P., Luhova L., Tsuno H.,
RA Hatata M., Amano Y., Kato Y., Matsushita K., Toyama H., Kumagai H.,
RA Adachi O.;
RT "Two distinct quinoxaline amine oxidases are induced by n-butylamine
in the mycelia of Aspergillus niger AKU 3302. Purification,
characterization, cDNA cloning and sequencing.";
RL Eur. J. Biochem. 237:255-265(1996).
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CC -----
DR PIR; S71304; S71304.
DR GO; GO:0008131; F:amine oxidase activity; IEA.
FT NON TER 1 1
SQ SEQUENCE 11 AA; 1158 MW; 21BBFDC44472DC7 CRC64;

Query Match 27.1%; Score 23; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 NSDP 5
Db 1 NSDP 4

RESULT 4
ID Q47602 ECOLI PRELIMINARY; PRT; 11 AA.
AC Q47602;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Rase protein (Fragment).
GN Name:Rase;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OK NCBI_TaxID=562;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91139577; PubMed=1995588;
RA Tao T., Bourne J.C., Blumenthal R.M.;
RT "A family of regulatory genes associated with type II restriction-
modification systems.";
RL J. Bacteriol. 173:1367-1375(1991).
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CC -----
DR EMBL; M63620; AAA24558.1; -; Genomic_DNA.
FT NON TER 11 11
SQ SEQUENCE 11 AA; 1412 MW; 80ABB190C736DAAA CRC64;

Query Match 25.9%; Score 22; DB 2; Length 11;
Best Local Similarity 44.4%; Pred. No. 1e+04;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 7 RTEQATW 15
Db 3 RDDQLFTW 11

RESULT 5
ID Q50117 MYCLE PRELIMINARY; PRT; 13 AA.
AC Q50117;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE U650W.
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OK NCBI_TaxID=1769;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RA Smith D.R.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
RN (2)
RP NUCLEOTIDE SEQUENCE.
RA Robison K.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; U15184; AAA63055.1; -; Genomic_DNA.
SQ SEQUENCE 13 AA; 1503 MW; CAABF1429D5412 CRC64;

Query Match 25.9%; Score 22; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.2e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 DSPVR 7
| | | |
Db 3 DEPV 7

RESULT 6

Q7M423_FUSSP PRELIMINARY; PRT: 15 AA.
AC Q7M423_15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 15-DEC-2003, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE Fumarate hydratase (EC 4.2.1.2) (Fragment).
OS Fusarium sporotrichioides.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
OX NCBI_TaxID=5514;
RN [1]
RP PROTEIN SEQUENCE.
RA Chow L.P., Fukaya N., Sugiyura Y., Ueno Y., Tabuchi K., Taugita A.;
RL Submitted (OCT-1994) to the PIR data bank.
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PIR: PA0062; PA0062.
DR GO; GO:0004333; F: fumarate hydratase activity; IEA.
FT NON TER 1 1
SQ SEQUENCE 15 AA; 1668 MW; 805CB18C239DE05 CRC64;

Query March 25.9%; Score 22; DB 2; Length 15;
Best Local Similarity 55.6%; Pred. No. 1.4e+04;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 SPVTEQQA 12
| | | |
Db 1 SQTRESDA 9

RESULT 7

Q9TS39_9PRIM PRELIMINARY; PRT: 15 AA.
AC Q9TS39_01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 7.
DE Dopamine D5 (Fragment).
OS Gorilla gorilla (Gorilla).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Gorilla.
OX NCBI_TaxID=9593;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92068184; PubMed=1958184;
RA Nguyen T., Sunahara R., Marchese A., Van Tol H.H., Seeman P.,
RA O'Dowd B.F.;
RT "Transcription of a human dopamine D5 pseudogene";
RL Biochem. Biophys. Res. Commun. 181:16-21(1991).
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FT NON TER 1 1
SQ SEQUENCE 15 AA; 1637 MW; 39D8326BA63BB90B CRC64;

Query March 25.3%; Score 21.5; DB 2; Length 15;
Best Local Similarity 33.3%; Pred. No. 1.8e+04;
Matches 5; Conservative 1; Mismatches 2; Indels 7; Gaps 1;

QY 1 HNDSPVTEQQAATTW 15

Db 1 HRD-----QAASM 8

RESULT 8

CWP06_PHAVU STANDARD; PRT: 9 AA.
ID CWP06_PHAVU
AC P80765;
DT 27-SEP-2005, integrated into UniProtKB/Swiss-Prot.
DT 27-SEP-2005, sequence version 1.
DT 07-MAR-2006, entry version 5.
DE 60 kDa cell wall protein (Fragment).
OS Phaseolus vulgaris (Kidney bean) (French bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
OC Phaseolus.
OX NCBI_TaxID=3885;
RN [1]
RP PROTEIN SEQUENCE, AND SUBCELLULAR LOCATION.
RX MEDLINE=97332671; PubMed=9188482; DOI=10.1074/jbc.272.25.15841;
RA Robertson D., Mitchell G.P., Gilroy J.S., Gerrish C., Bolwell G.P.,
RA Slabas A.R.;
RT "Differential extraction and protein sequencing reveals major
RT differences in patterns of primary cell wall proteins from plants";
RL J. Biol. Chem. 272:15841-15848(1997).
CC - SUBCELLULAR LOCATION: Secreted; cell wall.
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KW Cell wall; Direct protein sequencing.
FT CHAIN 1 9
FT NON TER 9 9
SQ SEQUENCE 9 AA; 1160 MW; 9270B1A9C32B5DDA CRC64;

Query March 24.7%; Score 21; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+06;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 TTM 15
| | | |
Db 7 TTM 9

RESULT 9

Q798K5_STRLI PRELIMINARY; PRT: 9 AA.
AC Q798K5_05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-FEB-2006, entry version 6.
DE AmlB protein (Fragment).
CN Name=amlB;
OS Streptomyces lividans.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=1916;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98332731; PubMed=9666116; DOI=10.1016/S0378-1119(98)00265-0;
RA Yin X.H., Gerbaud C., Franou F.X., Guetinau M., Violette M.J.;
RT "amlC, another amyloid-like gene maps close to the amlB locus in
RT Streptomyces lividans TK24";
RL Gene 215:171-180(1998).
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FT NON TER 9 9
SQ SEQUENCE 9 AA; 970 MW; F334C775A1A44871 CRC64;

Query Match 24.7%; Score 21; DB 2; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2.8e+06;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 NDSPVR 7
 :|||
 Db 4 NTSPAR 9

RESULT 10

O9R635 CHLTR PRELIMINARY; PRT; 9 AA.
 ID O9R635 CHLTR
 AC O9R635
 DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
 DT 01-MAY-2000, sequence version 1.
 DT 07-FEB-2006, entry version 8.
 DE Major outer membrane protein variable domain IV, MOMP VD IV (Fragment).
 DE Chlamydia trachomatis.
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=813;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=92040090; PubMed=1718870;
 RA Peterson E.M., Cheng X., Markoff B.A., Fielder T.J., de la Maza L.M.,
 RT "Functional and structural mapping of Chlamydia trachomatis species-
 RT specific major outer membrane protein epitopes by use of neutralizing
 RT monoclonal antibodies.";
 RL Infect. Immun. 59:4147-4153(1991).
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 CC
 DR PIR; S16034; S16034.
 FT NON_TER 1 1
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 976 MW; 96C1B041B7645361 CRC64;

Query Match 24.7%; Score 21; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+06;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 TTW 15
 :|||
 Db 1 TTW 3

RESULT 11

O4A3D9 OENOE PRELIMINARY; PRT; 10 AA.
 ID O4A3D9 OENOE
 AC O4A3D9
 DT 13-SEP-2005, integrated into UniProtKB/TrEMBL.
 DT 13-SEP-2005, sequence version 1.
 DT 07-FEB-2006, entry version 2.
 DE Cipl2 protein (Fragment).
 OS Name: cipl2; oeni (Leuconostoc oenos).
 OS Oenococcus oeni (Leuconostoc oenos).
 OC Bacteria; Firmicutes; Lactobacillales; Oenococcus.
 OX NCBI_TaxID=1247;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX STRAIN=IOB 8413;
 RA Grandvalet C., Couchehey F., Beltramo C., Guzzo J.;
 RT "CtR is the Master Regulator of Stress Response Gene Expression
 RT in Oenococcus oeni.";
 RL J. Bacteriol. 147:5614-5623(2005).
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 CC
 DR EMBL; AJ890337; CA165389.1; -; Genomic_DNA.
 FT NON_TER 10 10

SEQ SEQUENCE 10 AA; 1186 MW; 9693E6A5A45B5A CRC64;

Query Match 24.7%; Score 21; DB 2; Length 10;
 Best Local Similarity 60.0%; Pred. No. 1.4e+04;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 HNDSP 5
 :|||
 Db 4 YNDP 8

RESULT 12

O5EDJ3 LEGPN PRELIMINARY; PRT; 11 AA.
 ID O5EDJ3 LEGPN
 AC O5EDJ3
 DT 15-MAR-2005, integrated into UniProtKB/TrEMBL.
 DT 15-MAR-2005, sequence version 1.
 DT 07-FEB-2006, entry version 3.
 DE Putative acyl carrier protein (Fragment).
 DE Legionella pneumophila.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
 OC Legionellaceae; Legionella.
 OX NCBI_TaxID=446;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX STRAIN=02/41;
 RA Newton H.J., Hartland E.L.;
 RT "Subtractive hybridization reveals DNA fragments present in Legionella
 RT pneumophila, strain 02/41, and absent in Legionella micdadei, strain
 RT 02/42.";
 RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
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 CC
 DR EMBL; AY902880; AA83806.1; -; Genomic_DNA.
 FT NON_TER 1 1
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1159 MW; DCC78B8601ADC66 CRC64;

Query Match 24.7%; Score 21; DB 2; Length 11;
 Best Local Similarity 80.0%; Pred. No. 1.5e+04;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 9 EQOAT 13
 :|||
 Db 3 QOQAT 7

RESULT 13

EP65 HUMAN STANDARD; PRT; 13 AA.
 ID EP65 HUMAN
 AC P54963;
 DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
 DT 01-OCT-1996, sequence version 1.
 DT 07-FEB-2006, entry version 18.
 DE Erythrocyte 65 kDa protein (P65) (Fragment).
 OS Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP PROTEIN SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE.
 RX MEDLINE=90004678; PubMed=2507249;
 RA Hart G.W., Hattwanger R.S., Holt G.D., Kelly W.G.;
 RT "Nucleoplasmic and cytoplasmic glycoproteins.";
 RL Ciba Found. Symp. 145:102-118(1989).
 CC -1- SUBCELLULAR LOCATION: Cytoplasm.
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 CC
 DR GO; GO:0005737; C:cytoplasm; NAS.

```

KW Direct protein sequencing; Glycoprotein.
FT CHAIN <1 >13 Erythrocyte 65 kDa protein.
FT CARBOHYD 2 2 O-linked (GlcNAc).
FT NON_TER 1 1
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1300 MW; D08B73344C61A776 CRC64;

Query Match 24.7%; Score 21; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 1.9e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 DSPV 6
DB 1 DSPV 4

RESULT 14
Q9SB03 ORYSA PRELIMINARY; PRT; 13 AA.
AC Q9SB03;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DE 07-FEB-2006, entry version 12.
DE Waxy (Fragment).
GN Name=Waxy;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=98384837; PubMed=9718725;
RX Hirano H., Biguchi M., Sano Y.;
RT "A single base change altered the regulation of the Waxy gene at the
RT post-transcriptional level during domestication of rice.";
RL Mol. Biol. Evol. 15:978-987(1998).
CC -----
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CC -----
DR EMBL: AB008794; BAA32471.1; -; Genomic_DNA.
DR Gramene; Q9SB03; -.
DR GO: GO:0004373; F:glycogen (starch) synthase activity; IEP.
DR GO: GO:0005982; P:starch metabolism; IEP.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1281 MW; 999F8DEB570FC5A1 CRC64;

Query Match 24.7%; Score 21; DB 2; Length 13;
Best Local Similarity 45.5%; Pred. No. 1.9e+04;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 4 SPVTEQOAT 14
DB 2 SALTSQLATS 12

RESULT 15
Q7IGS6 GHYME PRELIMINARY; PRT; 14 AA.
AC Q7IGS6;
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DE 07-MAR-2006, entry version 8.
DE Cytochrome oxidase subunit I (Fragment).
OS Andrena n. sp. 'goth'.
OS Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apoidea; Aculeata; Apoidea;
OC Andrenidae; Andreninae; Andrena; Callandrena.
OX NCBI_TaxID=205171;
RN [1]

```

```

RP NUCLEOTIDE SEQUENCE.
RC STRAIN=96;
RX PubMed=16343953; DOI=10.1016/j.ympev.2005.10.003;
RA Larkin L.B., Neft U.L., Simpson B.B.;
RT "Phylogeny of the Callandrena subgenus of Andrena (Hymenoptera:
RT Andrenidae) based on mitochondrial and nuclear DNA data: Polyphyly and
RT convergent evolution.";
RL Mol. Phylogenet. Evol. 38:330-343(2006).
CC -----
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CC -----
DR EMBL: AF504376; AA007723.1; -; Genomic_DNA.
DR GO: GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1692 MW; 79E3B922A4E7B5B CRC64;

Query Match 24.7%; Score 21; DB 2; Length 14;
Best Local Similarity 37.5%; Pred. No. 2e+04;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPVTE 9
DB 6 NEIPIMTK 13

```

Search completed: May 30, 2006, 11:09:59
Job time : 72.3333 secs

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OM protein - protein search, using sw model

Run on: May 30, 2006, 09:58:50 ; Search time 60 Seconds
(without alignments)
114.304 Million cell updates/sec

Title: US-10-758-165A-2
Perfect score: 85
Sequence: 1 HNDSPVTEQQTW 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 837128

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_8:*

- 1: Geneseqp1980a:*
- 2: Geneseqp1990a:*
- 3: Geneseqp2000a:*
- 4: Geneseqp2001a:*
- 5: Geneseqp2002a:*
- 6: Geneseqp2003a:*
- 7: Geneseqp2003b:*
- 8: Geneseqp2004a:*
- 9: Geneseqp2005a:*
- 10: Geneseqp2006a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	85	100.0	15	8	ADRI0602 Cat IGE e
2	48	56.5	15	8	ADRI0601 Dog IGE e
3	39	46.9	15	8	ADRI0607 Pig IGE e
4	37	43.5	15	8	ADRI0603 Horse IGE
5	35	41.2	15	7	ADCI4568 Horse Imm
6	32	37.6	10	5	AAU79709 Synthetic
7	30	35.3	11	3	AAAB38098 Human ABC
8	29	34.1	6	4	AAAB55476 Human elA
9	29	34.1	15	2	AAAB55733 dedNA-dep
10	29	34.1	15	8	ADP97089 Cysteine
11	28.5	33.5	12	2	AAAB56548 Toxin fra
12	28	32.9	9	2	AAW76034 LM609 gra
13	28	32.9	9	4	AAAB61392 Mutant VL
14	28	32.9	9	6	ABO19830 Enhanced
15	28	32.9	9	6	ABR62303 Surface s
16	28	32.9	9	7	ADG71862 Enhanced
17	28	32.9	9	8	ADJ58043 Murine LM
18	28	32.9	9	8	ADL73181 CDR3 of t
19	28	32.9	10	5	ABG98755 F protein
20	28	32.9	13	2	AAAR79898 Fusion pr
21	28	32.9	15	7	ADW62941 Human 98P
22	28	32.9	15	7	ADW63829 Human 98P
23	27	31.8	8	2	AAWS9312 Non-polio

24	27	31.8	9	3	AAAB10015	AAAB10015 H. pylori
25	27	31.8	9	4	AAAB86095	AAAB86095 H. pylori
26	27	31.8	9	4	AAAB86063	AAAB86063 H. pylori
27	27	31.8	9	5	AAAB99231	AAAB99231 CD45RO/RB
28	27	31.8	9	5	AAU72845	AAU72845 Anti-NKG2
29	27	31.8	9	5	AAU72853	AAU72853 Anti-NKG2
30	27	31.8	9	9	ADY80269	ADY80269 CDR3 from
31	27	31.8	9	9	AED67669	AED67669 Humanized
32	27	31.8	9	10	AEED21780	AEED21780 Humanized
33	27	31.8	10	5	ABG98754	ABG98754 F protein
34	27	31.8	13	2	AAAB63411	AAAB63411 Peptide f
35	27	31.8	13	2	AAAB94483	AAAB94483 Hepatitis
36	27	31.8	14	4	AAAB97114	AAAB97114 Human pep
37	27	31.8	14	8	ADT40356	ADT40356 HSARS vir
38	27	31.8	14	8	ADT37886	ADT37886 HSARS vir
39	27	31.8	14	8	ADT37886	ADT37886 HSARS vir
40	26	30.6	8	2	AAAY04462	AAAY04462 Active mI
41	26	30.6	9	6	ABP74676	ABP74676 Human SCP
42	26	30.6	9	6	AAE38100	AAE38100 Human COU
43	26	30.6	9	7	ADCO9535	ADCO9535 Epitope w
44	26	30.6	9	8	ADN28303	ADN28303 Human CD3
45	26	30.6	10	2	AAAY04464	AAAY04464 Active mI

ALIGNMENTS

RESULT 1
ADRI0602
ID ADRI0602 standard; peptide: 15 AA.

AC ADRI0602;
XX
DT 21-OCT-2004 (first entry)

DE Cat IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 2.

KM Antiasthmatic; Antiallergic; Immunosuppressive; IGE; dog; asthma;
KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
KM cat.

OS Fells catue.
XX
PN WO2004065936-A2.

PD 05-AUG-2004.
XX
PF 15-JAN-2004; 2004WO-US003566.
XX
PR 16-JAN-2003; 2003US-0440472P.

(UYNC-) UNIV NORTH CAROLINA STATE.
XX
PA Hammerberg B;
XX
PI Hammerberg B;
XX
DR WPI; 2004-593545/57.

PT Novel antibody that specifically binds to mammalian IGE epitope, useful
PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE
PT or treating asthma or anaphylactic shock.

PS Example 6; Page 9; 14pp: English.

The present invention relates to a novel monoclonal antibody (I) that
specifically binds to a mammalian IGE epitope, where the epitope is
between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
(I) is useful for testing an allergen reactivity of an IGE sample. The
allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
and corn allergens. The sample is a biological sample collected from a
dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
antibodies recognise epitopes on canine IGE corresponding to amino acid
residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the

CC canine IgE epsilon-chain. Recognition of epsilon-chains from IgE from
CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
CC of IgE from cat and horse, but did not exhibit cross-reactivity with
CC either pig or human epsilon-chains of IgE. The present sequence is the
CC cat IgE 5.91 recognition site.

SQ Sequence 15 AA;

Query Match	100.0%;	Score 85;	DB 8;	Length 15;
Best Local Similarity	100.0%;	Pred. No. 6e-08;		
Matches 15; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0

QY	1	HNDS	PV	RT	EQ	QA	TT	W	15
Db	1	HNDS	PV	RT	EQ	QA	TT	W	15

RESULT 2
ADR10601

DT 21-OCT-2004 (first entry)

DE Dog IgE epitope recognised by monoclonal antibody 5.91, SEQ ID 1.

KM Antiasthmatic; Antiallergic; Immunosuppressive; IgE; dog; asthma;
KM anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody

OS Canis familiaris

PN WO2004065936-A2.

PD 05-AUG-2004

PF 15-JAN-2004; 2004WO-US003566.

PR 16-JAN-2003; 2003US-0440472P

PA (UYN-) UNIV NORTH CAROLINA STATE

PI Hammerberg B;

DR WPI; 2004-593545/57.

PT Novel antibody that specifically binds to mammalian IgE epitope, useful
PT for testing an allergen reactivity of IgE sample, detecting mammalian IgE
PT or treating asthma or anaphylactic shock.

PS Example 6; Page 9; 14pp; English.

The present invention relates to a novel monoclonal antibody (1) that specifically binds to a mammalian IgE epitope, where the epitope is between amino acids 145-166 or 355-374 of mammalian IgE, e.g. dog IgE. (1) is useful for testing an allergen reactivity of an IgE sample. The allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut and corn allergens. The sample is a biological sample collected from a dog, cat or horse. (1) is also useful for detecting mammalian IgE and for treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal antibodies recognize epitopes on canine IgE corresponding to amino acid residues 357-371 (ADRI10601) and 146-162 (ADRI10609) respectively of the canine IgE epsilon-chain. Recognition of epsilon-chains from IgE from cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and 3.76 were observed to have good cross-reactivity with the epsilon-chain of IgE from cat and horse, but did not exhibit cross-reactivity with either pig or human epsilon-chains of IgE.

SQ Sequence 15 AA;

Query Match	Score	DB	Length
Best Local Similarity	Pred. No.	0.24	
56.5%	48	8	15
61.5%			

	Matches	8; Conservative	3; Mismatches	2; Indels	0; Gaps	0;
Oy	2	NDSPRTEQQA	TT	14		
		::				
Db	2	NDSPIQTDQY	TTT	14		

Db 2 NDSPIQTDQYTTT 14

RESULT 3

ID ADR10607 standard; peptide; 15 AA.

AC ADR10607;

DT 21-OCT-2004 (first entry)

DE Pig IgE epitope recognised by monoclonal antibody 5.91, SEQ ID NO 7.

KW Antiasthmatic; Antiallergic; Immunosuppressive; IGE; dog; asthma;
KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
KW pig.

OS Sus scrofa.

PN W02004065936-A2.

PD 05-AUG-2004.

PF 15-JAN-2004; 2004WO-US003566

PR 16-JAN-2003; 2003US-0440472P

PA (UYN-) UNIV NORTH CAROLINA STATE.

PI Hammerberg B;

WPI; 2004-593545/57

PT Novel antibody that specifically binds to mammalian IgE epitope, useful
PT for testing an allergen reactivity of IgE sample, detecting mammalian IgE
PT or treating asthma or anaphylactic shock.

PS Example 6; Page 9; 14pp; English.

The present invention relates to a novel monoclonal antibody (I) that specifically binds to a mammalian IgE epitope, where the epitope is between amino acids 145-166 or 356-374 of mammalian IgE, e.g. dog IgE. (I) is useful for testing an allergen reactivity of an IgE sample. The allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut and corn allergens. The sample is a biological sample collected from a dog, cat or horse. (I) is also useful for detecting mammalian IgE and for treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal antibodies recognise epitopes on canine IgE corresponding to amino acid residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the canine IgE epsilon-chain. Recognition of epsilon-chains from IgE from cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and 3.76 were observed to have good cross-reactivity with the epsilon-chain of IgE from cat and horse, but did not exhibit cross-reactivity with either pig or human epsilon-chains of IgE. The present sequence is the pig IgE 5.91 recognition site.

Sequence 15 AA;

Query Match	45.9%	Score 39	DB 8	Length 15
Best Local Similarity	46.2%	Pred. No. 9.9		
Matches	6	Conservative	2	Indels 0
		Mismatches		Gaps 0

QY 2 NDSPV RTEQQATT 14

Db 2 NDAPVQADRHSTT 14

RESULT 4
ADR10603

```

ID ADR10603 standard; peptide; 15 AA.
XX
AC ADR10603;
XX
XX 21-OCT-2004 (first entry)
XX
DE Horse IGE epitope recognised by monoclonal antibody 5.91. SEQ ID 3.
XX
XX Antiaethmatic; Antiallergic; Immunosuppressive; IGE; dog; asthma;
KM anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
XX horse.
XX
XX Equus caballus.
XX
XX WO2004065936-A2.
XX
XX 05-AUG-2004.
XX
XX 15-JAN-2004; 2004WO-US003566.
XX
XX 16-JAN-2003; 2003US-0440472P.
XX
XX (VYNC-) UNIV NORTH CAROLINA STATE.
XX
XX Hammerberg B;
XX
XX WPI; 2004-593545/57.
XX
XX Novel antibody that specifically binds to mammalian IGE epitope, useful
PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE
PT or treating asthma or anaphylactic shock.
XX
XX Example 6; Page 9; 14pp; English.
XX
XX The present invention relates to a novel monoclonal antibody (I) that
CC specifically binds to a mammalian IGE epitope, where the epitope is
CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
CC (I) is useful for testing an allergen reactivity of an IGE sample. The
CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
CC and corn allergens. The sample is a biological sample collected from a
CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
CC antibodies recognise epitopes on canine IGE corresponding to amino acid
CC residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the
CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from
CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
CC of IGE from cat and horse, but did not exhibit cross-reactivity with
CC either pig or human epsilon-chains of IGE. The present sequence is the
CC horse IGE 5.91 recognition site.
XX
XX Sequence 15 AA;
XX
XX Query Match 43.5%; Score 37; DB 8; Length 15;
XX Best Local Similarity 53.8%; Pred. No. 23;
XX Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 2 NDSPTREQQAATT 14
XX : : : : :
Db 2 NNVALIQTDQAATT 14

```

```

XX
XX Equus caballus.
XX
XX US2003087314-A1.
XX
XX 08-MAY-2003.
XX
XX 08-NOV-2001; 2001US-00052788.
XX
XX 08-NOV-2001; 2001US-00052788.
XX
XX 08-NOV-2001; 2001US-00052788.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Gershwin LJ, Pettigrew HD, Kalina WV;
XX
XX WPI; 2003-765437/72.
XX
XX Immunogenic composition comprising an isolated equine immunoglobulin E
PT polypeptide that induces production of antibodies which specifically bind
PT to equine immunoglobulin E.
XX
XX Example 1; Page 8; 14pp; English.
XX
XX The invention relates to an immunogenic composition comprising an
CC isolated polypeptide having an amino acid sequence that is at least 80%
CC identical to 6 (S1-S6), 15 amino acid peptide sequences derived from
CC equine immunoglobulin E (the composition induces production of an
CC antibody that specifically binds to equine immunoglobulin (Ig)E), the six
CC polypeptides are not explicitly identified in the specification. Also
CC included are a composition comprising an antibody that specifically binds
CC to a polypeptide at least 80% identical to (S1)-(S6), an antibody that
CC specifically binds to equine IGE made by the process of immunising an
CC animal with a polypeptide at least 80% identical to (S1)-(S6), making an
CC antibody that specifically binds to equine IGE (involving immunising an
CC animal with a composition further comprising an isolated polypeptide (the
CC (S6)), and collecting antiserum from the animal) and a kit for detection
CC of equine IGE in a biological sample comprising the antibody and means
CC for detecting specific binding of the antibody to equine IGE. The
CC antibody is useful for detecting equine IGE protein in a biological
CC sample (serum) which involves contacting the sample with the antibody,
CC thus forming an antigen/antibody complex, and detecting the presence or
CC absence of the antigen/antibody complex. The antibody and antigen are
CC immobilised on a solid surface. The antibody is labelled such that the
CC complex can be detected. The complex is detected using a second labelled
CC antibody. The peptides are useful for generating antibodies specific for
CC IGE which can serve as a diagnostic test for allergy. The present
CC sequence is a Horse immunoglobulin E, IGE, heavy chain immunogenic
CC peptide from the early portion of the C4 region.
XX
XX Sequence 15 AA;
XX
XX Query Match 41.2%; Score 35; DB 7; Length 15;
XX Best Local Similarity 66.7%; Pred. No. 52;
XX Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 6 VRIEQQAATT 14
XX : : : : :
Db 1 IQTDQAATT 9

```

```

RESULT 6
AAU79709
ID AAU79709 standard; peptide; 11 AA.
XX
XX AAU79709;
XX
XX 15-JUL-2002 (first entry)
XX
XX Synthetic peptide CPP-2 used in invention of DRL90.
XX
XX Human; tissue-specific secretory polypeptide; DRU90; infection; cancer;
XX immune disease; digestive disease; circulatory disease;
XX

```

KM endocrine disease; infertility; cytostatic; immunomodulator;
KW antimicrobial; vasotropic; antiinfertility; hormonal; CPP-2.
XX
OS Synthetic.
XX
PN WO200224908-A1.
XX
PD 26-MAR-2002.
XX
PF 21-SEP-2001; 2001WO-JP008223.
XX
PR 22-SEP-2000; 2000JP-00293985.
XX 29-SEP-2000; 2000JP-00302839.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Ito Y, Tanaka H, Nishimura A, Ogi K;
XX
DR WPI; 2002-330018/36.
XX
PT New tissue-specific secretory polypeptides applicable in diagnosis of and
PT remedies for cancer, immune diseases, infection, digestive diseases,
PT circulatory diseases, endocrine diseases and infertility.
XX
PS Example 8; Page 80; 11pp; Japanese.
XX
CC The present invention relates to the isolation of a novel tissue-specific
CC secretory polypeptide, DRB90, and the polynucleotide sequence encoding
CC it. The DRB90 polypeptide and encoding DNA are useful for diagnosing and
CC treating cancer, immune diseases, infection, digestive diseases,
CC circulatory diseases, endocrine diseases and infertility. The present
CC sequence for synthetic peptide CPP-2 is used in the examples of the
CC present invention
XX
SQ Sequence 11 AA;
XX
Query Match 37.6%; Score 32; DB 5; Length 11;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX
QY 4 SPVTEQQA 12
||: ||: ||
2 SPILTEKQA 10
XX
RESULT 7
AAB38098
ID AAB38098 standard; peptide; 10 AA.
XX
AC AAB38098;
XX
DT 29-JAN-2001 (first entry)
XX
DE Human ABC1 FHA-3 mutant exon 41-encoded peptide fragment, SEQ ID NO:65.
XX
KM Human ABC1 cholesterol transporter; chromosome 9q11;
KM ATP-binding cassette; HDL deficiency disorder; high density lipoprotein;
KM Tangier disease; TD; familial HDL deficiency; FHA; polymorphism;
KM cardiovascular disease; coronary artery disease; coronary restenosis;
KM cerebrovascular disease; peripheral vascular disease;
KM Alzheimer's disease; Niemann-Pick disease; Huntington's disease;
KM X-linked adrenoleukodystrophy; cancer; gene therapy; genetic diagnosis;
KM prognosis; prophylaxis; drug screening; transgenic animal.
XX
OS Homo sapiens.
XX
PN WO200055318-A2.
XX
PD 21-SEP-2000.
XX
PF 15-MAR-2000; 2000WO-IB000532.
XX
PR 15-MAR-1999; 99US-0124702P.

PR 08-JUN-1999; 99US-0138048P.
PR 17-JUN-1999; 99US-0139600P.
PR 01-SEP-1999; 99US-0151977P.
XX
XX
PA (UYBR-) UNIV BRITISH COLUMBIA.
XX (XENO-) XENON BIORESEARCH INC.
XX
PI Hayden MR, Wilson AR, Pimstone SN;
XX
DR WPI; 2000-587528/55.
DR N-PSDB; AAC69168.
XX
PT New ABC1 polypeptide is useful for treating diseases associated with ABC1
PT biological activity, e.g. Alzheimer's disease, Huntington's disease and
PT cancer.
XX
PS Example; Fig 6E; 229pp; English.
XX
CC The invention relates to the human ABC1 cholesterol transporter protein
CC (B38082) and to nucleic acid sequences (CG9120) which encode it. ABC1 is
CC a member of the ATP-binding cassette (ABC transporter) superfamily of
CC proteins, and plays a crucial role in cholesterol transport, particularly
CC intracellular cholesterol trafficking in monocytes and fibroblasts, being
CC involved in cholesterol efflux from the cell. The gene encoding ABC1 is
CC located on chromosome 9q31, and mutations in this gene are associated
CC with two genetic HDL (high density lipoprotein) deficiency disorders,
CC Tangier disease (TD) and familial HDL deficiency (FHA). These diseases
CC are distinguishable in that TD is an autosomal recessive disorder, while
CC FHA is inherited as an autosomal dominant trait. Low levels of HDL ("good
CC cholesterol") in the blood correlate with a high risk of cardiovascular
CC disease, particularly coronary artery disease, but also cerebrovascular
CC disease, coronary restenosis, and peripheral vascular disease.
CC Conversely, a high level of HDL has protective effects against
CC cardiovascular disease. The invention provides genetic constructs and
CC transgenic cells and non-human animals comprising human ABC1 nucleic
CC acids, and methods of gene therapy for the treatment or prevention of
CC cardiovascular disease comprising the administration of an expression
CC vector encoding ABC1 or an active fragment thereof. The invention also
CC encompasses compounds which mimic ABC1 activity, compounds which
CC stimulate ABC1 expression and methods of screening for such compounds. It
CC further relates to methods for determining whether a patient has an
CC increased risk for cardiovascular disease due to polymorphisms in the
CC ABC1 gene. Human ABC1 proteins and nucleotides can be used to treat or
CC prevent cardiovascular disease, especially coronary artery disease,
CC cerebrovascular disease, coronary restenosis or peripheral vascular
CC disease. They may also be used in the treatment of diseases associated
CC with ABC1 biological activity, such as Alzheimer's disease, Niemann-Pick
CC disease, Huntington's disease, X-linked adrenoleukodystrophy and cancer.
CC The invention specifically excludes proteins with the exact amino acid
CC sequences of GenBank Accession No: CAA10005.1 and X75926, and the nucleic
CC acid with the exact sequence as GenBank Accession No: AJ012376.1. The
CC present sequence represents a human ABC1 cholesterol transporter peptide
CC fragment used in the exemplifications of the invention
XX
SQ Sequence 10 AA;
XX
Query Match 35.3%; Score 30; DB 3; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
XX
QY 2 NDSVPRTEQQ 11
||: ||: ||: ||
1 NDESVRRERQ 10
XX
RESULT 8
AAB55476
ID AAB55476 standard; peptide; 6 AA.
XX
AC AAB55476;
XX
DT 07-MAR-2001 (first entry)
XX

PF	29-NOV-1993;	93WO-HU000065.
XX		
PR	30-NOV-1992;	92US-00984293.
XX		
XX	(BIOS-)	BIO SIGNAL KUTATO FEJLESZTO KFT.
PA	(SYNT-)	SYNTHETIC PEPTIDES INC.
XX		
PI	Keri G, Hodges RS, Cachia PJ, Szederkenyi F, Horvath A, Balogh A;	
PI	Vadasz Z;	
DR	WPI; 1994-200194/24.	
XX		
XX	New fatty acyl-peptide conjugates for inhibiting cell proliferation -	
PI	more active than free peptide, partic. for treating tumours, virus-	
PI	infected cells, psoriasis, etc.	
XX		
PS	Disclosure; Fig 1; 45pp; English.	
XX		
CC	The peptides given in AAR5718-48 can each be conjugated through an amide	
CC	linkage with a polyunsaturated fatty acid moiety, such as docosahexaenoic	
CC	acid or eicosapentaenoic acid, to improve antiproliferative activity. The	
CC	deRNA-dependent kinase inhibitor given in AAR5713 competes with native	
CC	kinases associated with neoplastic cell proliferation or transformation,	
CC	psoriasis, etc. (Updated on 25-MAR-2003 to correct PN field.)	
XX		
SQ	Sequence 15 AA;	
Query Match	34.1%;	Score 29; DB 2; Length 15;
Best Local Similarity	40.0%;	Pred. No. 6,1e+02;
Matches	4; Conservative	4; Mismatches 2; Indels 0; Gaps 0;
QY	1 HNDSPVTEQ 10	
	: : : :	
DB	6 YNDVPMEEE 15	
RESULT 10		
ADR97089		
ID	ADR97089	standard; peptide; 15 AA.
XX		
AC	ADR97089;	
XX		
DT	02-DEC-2004	(first entry)
XX		
DE	Cysteine protease inhibitory protein fragment #2.	
XX		
XX	antiinflammatory; vasotropic; immunostimulator;	
KW	cysteine protease inhibitory protein; diagnosis; Behcet's disease;	
XX	Harada's disease.	
XX		
OS	Homo sapiens.	
XX		
XX	MO2004078975-A1.	
PN		
XX		
PD	16-SEP-2004.	
XX		
PF	05-MAR-2004; 2004WO-JP002902.	
XX		
PR	05-MAR-2003; 2003JP-00059082.	
XX		
XX	(SENP) SENJU PHARM CO LTD.	
PA		
XX	Katunuma N, Shiota H;	
PI		
XX	WPI; 2004-668624/65.	
DR		
XX		
PT	Novel cysteine protease inhibitory protein, useful as diagnostic marker	
PI	for diagnosing Behcet's disease and Harada's disease.	
XX		
PS	Disclosure; SEQ ID NO 4; 64pp; Japanese.	
XX		
CC	A cysteine protease inhibitory protein (I) having the amino acid sequence	
CC	ADR97086 at its N-terminal and exhibiting the molecular weight of 31 kDa,	

is new. (1) is useful for screening a compound or its salt having activity of promoting or inhibiting the function of (1). (1) enables diagnosis, prevention or treatment of Bence's disease or Harada's disease. This sequence is a fragment of the cysteine protease inhibitory protein.

Sequence 15 AA;

Query Match 34.1%; Score 29; DB 8; Length 15;
 Best Local Similarity 38.5%; Pred. No. 6.1e+02;
 Matches 5; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

3 DSPVTEQQTW 15
 3 DRPARHPEQPLW 15

RESULT 11
 AAM56548
 ID AAM56548 standard; peptide; 12 AA.

AAW56548;
 AAW56548;
 07-AUG-1998 (first entry)

Toxin fragment of Tcac of the bacterium *Photorhabdus luminescens*.

Photorhabdus luminescens W-14, nematode, symbiotic; *Heterorhabditis*; tca; tcd; tcc; tcd; insecticidal activity; toxin; Lepidoptera; Coleoptera; Hymenoptera; Diptera; Dictyoptera; Acarina; Homoptera; Southern; Western corn rootworm; Colorado potato beetle; mealworm; boll weevil; turf grub; beetle armyworm; black cutworm; cabbage looper; codling moth; corn earworm; European corn borer; Tobacco hornworm; budworm.

Photorhabdus luminescens.
 WO9808932-A1.

05-MAR-1998.
 05-MAY-1997; 97WO-US007657.
 28-AUG-1996; 96US-00705484.
 06-NOV-1996; 96US-00743699.
 06-NOV-1996; 96WO-US018003.

(DOMC) DOWELANCO.
 (WISC) WISCONSIN ALUMNI RES FOUND.

Ensign JC, Bowen DJ, Petell J, Fatic R, Schoonover S;
 Firench-Constant RH, Rochelleau TA, Blackburn MB, Hey TD, Merlo DJ;
 Orr GL, Roberts JL, Strickland JA, Guo L, Ciche TA, Sukhapinda K;
 WPI; 1998-179427/16.

Isolated toxins from *Photorhabdus luminescens* strains - useful for control of insect pests.

Claim 30; Page 151; 32pp; English.

The present sequence represents a fragment of the toxic protein Tcac (encoded by gene tcaC) of the bacterium *Photorhabdus luminescens* (W-14). This is a symbiotic bacterium of the nematodes of the *Heterorhabditis* genus. The bacterium has at least 4 distinct genomic regions, tca, tcd, tcc, and tcd. Peptide products are produced from these regions that are associated with insecticidal activity. The native toxins are secreted proteins. The proteins are toxic to insects upon exposure and especially when ingested. The nucleic acid sequence can be used to produce transgenic plants, baculoviruses or microbial hosts for toxin production. They can be used to control insects pests from the lepidoptera, Coleoptera, Hymenoptera, Diptera, Dictyoptera, Acarina or Homoptera orders, especially the Southern or Western corn rootworm, Colorado potato beetle, mealworm, boll weevil, turf grub, beetle armyworm, black cutworm,

cabbage looper, codling moth, corn earworm, European corn borer or tobacco hornworm or budworm

Sequence 12 AA;

Query Match 33.5%; Score 28.5; DB 2; Length 12;
 Best Local Similarity 53.8%; Pred. No. 5.8e+02;
 Matches 7; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

3 DSPVTEQQTW 15
 3 DSP---EVSITW 12

RESULT 12
 AAW76034
 ID AAW76034 standard; protein; 9 AA.

AAW76034;
 AAW76034;
 02-NOV-1998 (first entry)

LM609 grafted antibody V-L region CDR3 protein fragment #3.

Vitaxin; antibody; variable region; heavy chain; light chain; integrin; LM609; inhibitor; integrin-mediated signal transduction; treatment; diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy; neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine; macular degeneration; osteoporosis; primer; V-L region; CDR; complementarity determining region.

Mue sp.
 WO9833919-A2.

06-AUG-1998.
 30-JAN-1998; 98WO-US001826.
 30-JAN-1997; 97US-00791391.

(IXSY-) IXSYS INC.
 Huse WD, Glaser SM;
 WPI; 1998-437472/37.
 N-PSDB; AAV49871.

Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3 integrin - and related grafted antibodies based on murine monoclonal LM609, also related nucleic acid, used to treat, prevent or diagnose angiogenesis or restenosis.

Claim 62; Page 41; 129pp; English.

AAW76007-W76040 are protein fragments of the grafted monoclonal antibody LM609 heavy and light chain variable region. LM609 and the antibody vitaxin bind selectively to integrin alphaVbeta3 and can be used to inhibit binding of alphavbeta3 to a ligand and thus block integrin-mediated signal transduction. This is useful in the treatment, prevention and diagnosis of alphavbeta3-mediated disease, specifically angiogenesis and restenosis (but also e.g. (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis etc.). The antibodies contain non-murine framework regions so are suitable for use in humans. Enhanced types of LM609 have affinity more than 90 times greater than that of parent the parent antibody

Sequence 9 AA;

Query Match 32.9%; Score 28; DB 2; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2.1e+06;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 10 QOATW 15
 ||:|
 Db 1 QOSTSW 6

RESULT 13

AAB61392 standard; peptide; 9 AA.

AC AAB61392;

DT 03-APR-2001 (first entry)

DE Mutant VL CDR3 peptide #2.

KM LM609; grafted antibody; alphaVbeta_3 integrin; angiogenesis;
 inflammatory; cancer; retina; restenosis; osteoporosis.

OS Unidentified.

PN WO200078815-A1.

PD 28-DEC-2000.

PF 23-JUN-2000; 2000WO-US017454.

PR 24-JUN-1999; 99US-00339922.

PA (MOLE-) APPLIED MOLECULAR EVOLUTION.

PI Huse WD, Wu H;

DR WPI; 2001-050110/06.

PT Enhanced LM609 grafted antibodies exhibiting selective binding affinity
 to alpha(V)beta(3) integrin, useful in the diagnosis and treatment of
 angiogenesis, inflammatory diseases e.g. psoriasis, cancers and
 osteoporosis.

PS Disclosure; Page 41; 132pp; English.

CC The present invention relates to enhanced LM609 grafted antibodies
 exhibiting selective binding affinity to alphaVbeta_3 integrin or their
 functional fragments. The antibodies or their functional fragments can be
 used in the diagnosis and treatment of alphaVbeta_3-mediated diseases
 such as angiogenesis, inflammatory diseases (such as psoriasis and
 chronic articular rheumatism), disorders associated with inappropriate or
 inappropriate invasion of vessels (such as diabetic retinopathy, Kaposi's
 neovascular glaucoma and cancer disorders such as tumours and
 sarcoma), retinal diseases (such as macular degeneration), restenosis and
 osteoporosis

SO Sequence 9 AA;

Query Match 32.9%; Score 28; DB 4; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2.1e+06;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 10 QOATW 15
 ||:|
 Db 1 QOSTSW 6

RESULT 14

ABO19830 standard; peptide; 9 AA.

AC ABO19830;

DT 28-AUG-2003 (first entry)

DE Enhanced LM609 light chain variable region CDR3 #2.

XX LM609; antibody; grafted antibody; alpha_vbeta_3; angiogenesis; CDR;
 KW alpha_vbeta_3-mediated disease; complementarity determining region;
 KM restenosis.

OS Unidentified.

PN US2003028009-A1.

PD 06-FEB-2003.

PF 06-JUL-2001; 2001US-00900590.

PR 30-JAN-1998; 98US-00016061.

PA (IXSY-) IXSYS INC.

PI Huse WD;

DR WPI; 2003-492042/46.

DR N-PSDB; ACD30189.

PT New Vitaxin or LM609 grafted antibody exhibiting selective binding
 affinity to alphaVbeta3, useful for treating an alphaVbeta3-mediated
 disease e.g., angiogenesis or restenosis.

PS Claim 65; Page 12; 71pp; English.

CC The invention relates to a Vitaxin or LM609 grafted antibody, exhibiting
 selective binding affinity to alpha_vbeta_3. The Vitaxin or LM609 grafted
 antibody is useful for treating an alpha_vbeta_3-mediated disease e.g.
 angiogenesis or restenosis. The present sequence represents the amino
 acid sequence of a LM609 complementarity determining region

SO Sequence 9 AA;

Query Match 32.9%; Score 28; DB 6; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2.1e+06;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 10 QOATW 15
 ||:|
 Db 1 QOSTSW 6

RESULT 15
 ABR62303 standard; peptide; 9 AA.

AC ABR62303;

DT 22-SEP-2003 (first entry)

DE Surface stimulation synthetic peptide useful in HIV-1 vaccine.

KM Surface stimulation synthetic peptide; SSSP; HIV-1; vaccine; anti-HIV;

KW vitucide; epitope.

OS Human immunodeficiency virus 1.

PN WO2003048186-A2.

PD 12-JUN-2003.

PF 23-NOV-2002; 2002WO-US037664.

PR 01-DEC-2001; 2001US-00012806.

PA (CREV/) CREVECOEUR H.

PI Crevecoeur H;

DR WPI; 2003-558941/52.

XX Configuration of synthetic peptides useful for treating hyper-variable
PT viral pathogen e.g. HIV, involves identifying non-sequential conserved
PT residues in selected viral proteins and designing a sequence from image
PT scan of the residues.

XX
PS Disclosure; Page 27; 55pp; English.

XX
CC The present sequence is that of a surface simulation synthetic peptide
CC (SSSP) corresponding to a non-sequential conserved residue epitope of HIV
CC -1 glycoprotein gp120 required for viral pathogenicity. It is an example
CC of SSSPs of the invention, which incorporate amino acid sequences that
CC simulate the 3-dimensional spatial positions of non-sequential conserved
CC residues necessary for viral pathogenicity. The SSSPs are useful for
CC incorporation into vaccines effective in eliciting an effective broad
CC spectrum immune response against hyper-variable viral pathogens such as
CC HIV-1, and in diagnostic kits. SSSPs provide a reliable strategy for
CC allowing the immune system to process and recognise discontinuous
CC epitopes and to mount immune responses to the 3-dimensional
CC configurations of targeted proteins

XX
SQ Sequence 9 AA;

Query Match 32.9%; Score 28; DB 6; Length 9;
Best Local Similarity 62.5%; Pred. No. 2.1e+06;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 SPVATEQO 11
: |||:
Db 1 NPCRTEKO 8

Search completed: May 30, 2006, 10:12:40
Job time : 62 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 30, 2006, 10:21:55 ; Search time 47 Seconds
(without alignments)
147.835 Million cell updates/sec

Title: US-10-758-165A-2
Perfect score: 85
Sequence: 1 HNSDPVTEQOATW 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 395127

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
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2: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/us08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/us09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/us10_PUBCOMB.pep:*
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6: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/us11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	85	100.0	15	5	US-10-758-165-2
2	48	56.5	15	5	US-10-758-165-1
3	39	45.9	15	5	US-10-758-165-7
4	37	43.5	15	5	US-10-758-165-3
5	35	41.2	15	4	US-10-052-788-4
6	32	37.6	11	4	US-10-381-089-18
7	32	37.6	15	4	US-10-381-089-8
8	30	35.3	10	4	US-10-452-510-65
9	30	35.3	10	4	US-10-617-334-65
10	30	35.3	10	4	US-10-744-465-65
11	30	35.3	10	4	US-10-833-679-65
12	30	35.3	10	5	US-10-818-279-65
13	28.5	33.5	12	4	US-10-262-794A-2
14	28	32.9	9	3	US-09-900-590-88
15	28	32.9	9	4	US-10-012-806A-39
16	28	32.9	9	4	US-10-305-231-88
17	28	32.9	9	4	US-10-463-847-88
18	28	32.9	10	4	US-10-432-234A-250
19	27	31.8	9	3	US-09-842-776A-39
20	27	31.8	9	4	US-10-239-656-31
21	27	31.8	9	4	US-10-239-656-41
22	27	31.8	9	4	US-10-467-546-21
23	27	31.8	9	5	US-10-666-332-21
24	27	31.8	9	6	US-11-108-135-12
25	27	31.8	9	6	US-11-126-978-12
26	27	31.8	10	4	US-10-432-234A-249
27	27	31.8	13	3	US-09-851-138-166

28	27	31.8	13	3	US-09-899-046-244	Sequence 244, App
29	27	31.8	13	3	US-09-878-481-244	Sequence 244, App
30	27	31.8	13	3	US-09-873-224-244	Sequence 244, App
31	27	31.8	14	5	US-10-808-187-1344	Sequence 1344, App
32	27	31.8	14	5	US-10-807-807-1344	Sequence 1344, App
33	27	31.8	14	6	US-11-004-399-2037	Sequence 2037, App
34	26	30.6	9	4	US-10-117-937-560	Sequence 560, App
35	26	30.6	9	4	US-10-428-335-103	Sequence 19, App
36	26	30.6	9	5	US-10-883-020-19	Sequence 19, App
37	26	30.6	9	6	US-11-067-064-560	Sequence 560, App
38	26	30.6	9	6	US-11-067-159-560	Sequence 560, App
39	26	30.6	9	6	US-11-203-251A-10	Sequence 10, App
40	26	30.6	9	6	US-11-203-251A-75	Sequence 75, App
41	26	30.6	10	3	US-09-908-332-53	Sequence 53, App
42	26	30.6	10	3	US-09-783-931-53	Sequence 53, App
43	26	30.6	10	4	US-10-117-937-561	Sequence 561, App
44	26	30.6	10	5	US-10-659-207-436	Sequence 436, App
45	26	30.6	10	5	US-10-929-988-436	Sequence 436, App

ALIGNMENTS

```
RESULT 1
US-10-758-165-2
; Sequence 2, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammettberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Felis catus
US-10-758-165-2

Query Match      100.0%  Score 85;  DB 5;  Length 15;
Best Local Similarity 100.0%;  Pred. No. 7e+08;
Matches 15;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Oy      1  HNSDPVTEQOATW 15
      |||
Db      1  HNSDPVTEQOATW 15

RESULT 2
US-10-758-165-1
; Sequence 1, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammettberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US/10/758,165
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-758-165-1

Query Match      56.5%  Score 48;  DB 5;  Length 15;
```

Best Local Similarity 61.5%; Pred. No. 0.25;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSFVTEQOATT 14
|:|:|:|:|
Db 2 NDSFQTDQYTTT 14

RESULT 3

US-10-758-165-7
; Sequence 7, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; PRIOR FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Sus scrofa
US-10-758-165-7

Query Match 45.9%; Score 39; DB 5; Length 15;
Best Local Similarity 46.2%; Pred. No. 10;
Matches 6; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSFVTEQOATT 14
|:|:|:|:|
Db 2 NDAFVQADRHSTT 14

RESULT 4

US-10-758-165-3
; Sequence 3, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Equus caballus
US-10-758-165-3

Query Match 43.5%; Score 37; DB 5; Length 15;
Best Local Similarity 53.8%; Pred. No. 23;
Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSFVTEQOATT 14
|:|:|:|:|
Db 2 NNVLQTDQOATT 14

RESULT 5

US-10-052-788-4
; Sequence 4, Application US/10052788
; Publication No. US2003008731A1
; GENERAL INFORMATION:
; APPLICANT: Gettswin, Laurel J.
; APPLICANT: Pettigrew, Howard David

; APPLICANT: Kalina, Warren V.
; TITLE OF INVENTION: Epsilon Immunoglobulin Chain Derived Peptides for
; TITLE OF INVENTION: Induction of Anti-IgE Antibodies
; FILE REFERENCE: 023070-121000US
; CURRENT APPLICATION NUMBER: US/10/052,788
; CURRENT FILING DATE: 2001-11-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: epitope peptide
; OTHER INFORMATION: P4, early portion of C4 of equine IgE epsilon
US-10-052-788-4

Query Match 41.2%; Score 35; DB 4; Length 15;
Best Local Similarity 66.7%; Pred. No. 51;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 6 VTEQOATT 14
|:|:|:|:|
Db 1 IQTDQOATT 9

RESULT 6

US-10-381-089-18
; Sequence 18, Application US/10381089
; Publication No. US20040053276A1
; GENERAL INFORMATION:
; APPLICANT: ITO, Yasuaki
; APPLICANT: TANAKA, Hideyuki
; APPLICANT: NISHIMURA, Atsushi
; APPLICANT: OGI, Kazuhito
; TITLE OF INVENTION: Tissue specific novel secretory polypeptide and its DNA
; FILE REFERENCE: 2789 USOP
; CURRENT APPLICATION NUMBER: US/10/381,089
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2000-293985
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: JP 2000-302839
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 18
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide CPP1-2
US-10-381-089-18

Query Match 37.6%; Score 32; DB 4; Length 11;
Best Local Similarity 66.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 SPVTEQQA 12
|:|:|:|:|
Db 2 SPVTEKQA 10

RESULT 7

US-10-381-089-8
; Sequence 8, Application US/10381089
; Publication No. US20040053276A1
; GENERAL INFORMATION:
; APPLICANT: ITO, Yasuaki
; APPLICANT: TANAKA, Hideyuki
; APPLICANT: NISHIMURA, Atsushi
; APPLICANT: OGI, Kazuhito
; TITLE OF INVENTION: Tissue specific novel secretory polypeptide and its DNA

FILE REFERENCE: 2789 USOP
; CURRENT APPLICATION NUMBER: US/10/381,089
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: JP 2000-293985
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: JP 2000-302839
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 8
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human
US-10-381-089-8

Query Match 37.6%; Score 32; DB 4; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 SPVTEQQA 12
||: ||: ||
Db 1 SPILTEKQA 9

RESULT 8
US-10-452-510-65
; Sequence 65, Application US/10452510
; Publication No. US2004005666A1
; GENERAL INFORMATION:
; APPLICANT: Hayden, Michael R.
; APPLICANT: Brooks-Wilson, Angela R.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING CHOLESTEROL LEVELS
; FILE REFERENCE: 760050-93
; CURRENT APPLICATION NUMBER: US/10/452,510
; CURRENT FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: US 09/526,193
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 60/124,702
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: 60/138,048
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: 60/139,600
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: 60/151,977
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 287
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-452-510-65

Query Match 35.3%; Score 30; DB 4; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 NDSFVTEQQ 11
||: ||: ||
Db 1 NDEVRERQQ 10

RESULT 9
US-10-617-334-65
; Sequence 65, Application US/10617334
; Publication No. US20040058869A1
; GENERAL INFORMATION:
; APPLICANT: Hayden, Michael R.
; APPLICANT: Brooks-Wilson, Angela R.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING CHOLESTEROL LEVELS
; FILE REFERENCE: 760050-91
; CURRENT APPLICATION NUMBER: US/10/617,334
; CURRENT FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: US 09/526,193

PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 60/124,702
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: 60/138,048
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: 60/139,600
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: 60/151,977
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 287
; SOFTWARE: PatentIn 3.0
; SEQ ID NO 65
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-617-334-65

Query Match 35.3%; Score 30; DB 4; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 NDSFVTEQQ 11
||: ||: ||
Db 1 NDEVRERQQ 10

RESULT 10
US-10-744-465-65
; Sequence 65, Application US/10744465
; Publication No. US20040157250A1
; GENERAL INFORMATION:
; APPLICANT: Hayden, Michael R.
; APPLICANT: Brooks-Wilson, Angela R.
; APPLICANT: Plimstone, Simon N.
; TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING CHOLESTEROL LEVELS
; FILE REFERENCE: 760050-92
; CURRENT APPLICATION NUMBER: US/10/744,465
; CURRENT FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: 10/617,334
; PRIOR FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: US 09/526,193
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: 60/124,702
; PRIOR FILING DATE: 1999-03-15
; PRIOR APPLICATION NUMBER: 60/138,048
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: 60/139,600
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: 60/151,977
; PRIOR FILING DATE: 1999-09-01
; NUMBER OF SEQ ID NOS: 287
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-744-465-65

Query Match 35.3%; Score 30; DB 4; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 NDSFVTEQQ 11
||: ||: ||
Db 1 NDEVRERQQ 10

RESULT 11
US-10-833-679-65
; Sequence 65, Application US/10833679
; Publication No. US20040185508A1
; GENERAL INFORMATION:
; APPLICANT: Hayden, Michael R.

APPLICANT: Brooks-Wilson, Angela R.
APPLICANT: Pimstone, Simon N.
TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING CHOLESTEROL LEVELS
FILE REFERENCE: 760050-135
CURRENT APPLICATION NUMBER: US/10/833,679
PRIOR FILING DATE: 2004-04-28
PRIOR APPLICATION NUMBER: 10/452,510
PRIOR FILING DATE: 2003-06-02
PRIOR APPLICATION NUMBER: 10/617,334
PRIOR FILING DATE: 2003-07-10
PRIOR APPLICATION NUMBER: 09/526,193
PRIOR FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: 60/124,702
PRIOR FILING DATE: 1999-03-15
PRIOR APPLICATION NUMBER: 60/138,048
PRIOR FILING DATE: 1999-06-08
PRIOR APPLICATION NUMBER: 60/139,600
PRIOR FILING DATE: 1999-06-17
PRIOR APPLICATION NUMBER: 60/151,977
PRIOR FILING DATE: 1999-09-01
NUMBER OF SEQ ID NOS: 287
SOFTWARE: Patentin 3.0
SEQ ID NO 65
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-10-833-679-65

Query Match 35.3%; Score 30; DB 4; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 2 NDSVRTREQ 11
DB 1 NDEDVRRERQ 10

RESULT 12
US-10-818-279-65
Sequence 65, Application US/10818279
Publication No. US20050136421A1
GENERAL INFORMATION:
APPLICANT: Hayden, Michael R.
APPLICANT: Brooks-Wilson, Angela R.
APPLICANT: Pimstone, Simon N.
TITLE OF INVENTION: METHODS AND REAGENTS FOR MODULATING CHOLESTEROL LEVELS
FILE REFERENCE: 760050-126
CURRENT APPLICATION NUMBER: US/10/818,279
CURRENT FILING DATE: 2004-04-05
PRIOR APPLICATION NUMBER: 10/745,377
PRIOR FILING DATE: 2003-12-23
PRIOR APPLICATION NUMBER: 10/617,334
PRIOR FILING DATE: 2003-07-10
PRIOR APPLICATION NUMBER: 09/526,193
PRIOR FILING DATE: 2000-03-15
PRIOR APPLICATION NUMBER: 60/124,702
PRIOR FILING DATE: 1999-03-15
PRIOR APPLICATION NUMBER: 60/138,048
PRIOR FILING DATE: 1999-06-08
PRIOR APPLICATION NUMBER: 60/139,600
PRIOR FILING DATE: 1999-06-17
PRIOR APPLICATION NUMBER: 60/151,977
PRIOR FILING DATE: 1999-09-01
NUMBER OF SEQ ID NOS: 287
SOFTWARE: Patentin 3.0
SEQ ID NO 65
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-10-818-279-65

Query Match 35.3%; Score 30; DB 5; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.5e+02;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 2 NDSVRTREQ 11
DB 1 NDEDVRRERQ 10

RESULT 13
US-10-262-794A-2
Sequence 2, Application US/10262794A
Publication No. US2003020786A1
GENERAL INFORMATION:
APPLICANT: Ensign, Jerald C
APPLICANT: Bowen, David J
APPLICANT: Petell, James
APPLICANT: Fatig, Raymond
APPLICANT: Schoonover, Sue
APPLICANT: French-Constant, Richard
APPLICANT: Rocheleau, Thomas A.
APPLICANT: Blackburn, Michael B.
APPLICANT: Hey, Timothy D.
APPLICANT: Merlo, Donald J.
APPLICANT: Orr, Gregory L.
APPLICANT: Roberts, Jean L.
APPLICANT: Strickland, James A.
APPLICANT: Guo, Lining
APPLICANT: Cliche, Todd A.
APPLICANT: Sukhupinda, Kitieri
TITLE OF INVENTION: Insecticidal Protein Toxins From Photorhabdus
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dow Agrosciences Patent Department
STREET: 9330 Zionsville Road
CITY: Indianapolis
STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/262,794A
FILING DATE: 02-OCT-2002
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,567
FILING DATE: 05-MAY-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/063,615
FILING DATE: 18-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/395,497
FILING DATE: 28-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/007,255
FILING DATE: 06-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/608,423
FILING DATE: 28-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/705,484
FILING DATE: 28-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296,93804
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: N-terminal
US-10-262-794A-2

Query Match 33.5%; Score 28.5; DB 4; Length 12;
Best Local Similarity 53.8%; Pred. No. 5.7e+02;

Matches 7; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

QY 3 DSPVTEQQTW 15
DB 3 DSP---EVSITW 12

RESULT 14

US-09-900-590-88
Sequence 88, Application US/09900590
Publication No. US20030028009A1
GENERAL INFORMATION:

APPLICANT: Huse, William D.
Glaeser, Scott M.

TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
Antibodies, Nucleic Acids Encoding Same and Methods of Use

NUMBER OF SEQUENCES: 100

CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP

STREET: 4370 La Jolla Village Drive, Suite 700

CITY: San Diego

STATE: California

COUNTRY: United States

ZIP: 92122

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/900,590

FILING DATE: 06-Jul-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/016,061

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-IX 2965

TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001

TELEFAX: (619) 535-8949

INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 88:
US-09-900-590-88

Query Match 32.9%; Score 28; DB 3; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.9e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 QQATTW 15
DB 1 QQSTSW 6

RESULT 15

US-10-012-806A-39

Sequence 39, Application US/10012806A
Publication No. US20030125518A1
GENERAL INFORMATION:

APPLICANT: CREVICOUER, HARRY

TITLE OF INVENTION: SURFACE SIMULATION SYNTHETIC PEPTIDES USEFUL IN THE
TREATMENT OF HYPER-VARIABLE VIRAL PATHOGENS

FILE REFERENCE: 2001-Crev1

CURRENT APPLICATION NUMBER: US/10/012,806A

NUMBER OF SEQ ID NOS: 45

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 39

LENGTH: 9

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic
peptide

US-10-012-806A-39

Query Match 32.9%; Score 28; DB 4; Length 9;
Best Local Similarity 62.5%; Pred. No. 1.9e+06;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 SPVTEQQT 11
DB 1 NPCRTERQ 8

Search completed: May 30, 2006, 10:24:41

Job time : 48 secs

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OM protein - protein search, using sw model

Run on: May 30, 2006, 10:22:25 ; Search time 5.66667 Seconds
(without alignments)
29.481 Million cell updates/sec

Title: US-10-758-165A-2

Perfect score: 85
Sequence: 1 HNDSPVTEQATW 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 1113735 residues

Total number of hits satisfying chosen parameters: 10973

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Published Applications AA New:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	31.8	9	US-11-297-317-21	Sequence 21, App1
2	26	30.6	9	US-11-140-487A-1220	Sequence 1220, App
3	25	29.4	14	US-11-122-986-778	Sequence 778, App
4	23	27.1	10	US-10-538-066-163	Sequence 163, App
5	22	25.9	7	US-10-489-071-6	Sequence 6, App1
6	22	25.9	11	US-10-546-594-92	Sequence 92, App1
7	21	24.7	9	US-11-140-487A-1766	Sequence 1766, App
8	21	24.7	10	US-10-516-079-64	Sequence 64, App1
9	20	23.5	9	US-11-023-959A-63	Sequence 63, App1
10	20	23.5	11	US-10-981-300-34	Sequence 34, App1
11	20	23.5	12	US-11-106-014-84	Sequence 84, App1
12	20	23.5	15	US-11-140-487A-2207	Sequence 2207, App
13	19	22.4	8	US-10-538-066-404	Sequence 404, App
14	19	22.4	9	US-10-538-066-159	Sequence 159, App
15	19	22.4	9	US-10-538-066-429	Sequence 429, App
16	19	22.4	9	US-11-023-959A-18	Sequence 18, App1
17	19	22.4	9	US-11-023-959A-36	Sequence 36, App1
18	19	22.4	9	US-11-023-959A-51	Sequence 51, App1
19	19	22.4	9	US-11-023-959A-72	Sequence 72, App1
20	19	22.4	9	US-11-332-378-76	Sequence 76, App1
21	19	22.4	10	US-10-538-066-184	Sequence 184, App
22	19	22.4	10	US-10-538-066-268	Sequence 268, App
23	19	22.4	10	US-10-538-066-413	Sequence 413, App
24	19	22.4	10	US-10-538-066-415	Sequence 415, App
25	19	22.4	11	US-10-538-066-393	Sequence 393, App

26	19	22.4	11	US-10-538-066-414	Sequence 414, App
27	19	22.4	12	US-10-538-066-381	Sequence 381, App
28	19	22.4	13	US-11-121-382-197	Sequence 197, App
29	19	22.4	15	US-11-140-487A-2231	Sequence 2231, App
30	18	21.2	6	US-10-525-126-33	Sequence 33, App1
31	18	21.2	7	US-10-522-043-2	Sequence 2, App1
32	18	21.2	8	US-11-213-668-74	Sequence 74, App1
33	18	21.2	9	US-10-538-066-174	Sequence 174, App
34	18	21.2	9	US-10-538-066-299	Sequence 299, App
35	18	21.2	9	US-11-140-487A-895	Sequence 895, App
36	18	21.2	9	US-11-140-487A-1042	Sequence 1042, App
37	18	21.2	9	US-11-140-487A-1377	Sequence 1377, App
38	18	21.2	9	US-11-140-487A-1561	Sequence 1561, App
39	18	21.2	9	US-11-140-487A-1767	Sequence 1767, App
40	18	21.2	10	US-10-489-266-20	Sequence 20, App1
41	18	21.2	10	US-10-538-066-172	Sequence 172, App
42	18	21.2	10	US-10-538-066-267	Sequence 267, App
43	18	21.2	10	US-11-140-487A-1378	Sequence 1378, App
44	18	21.2	10	US-11-140-487A-1768	Sequence 1768, App
45	18	21.2	10	US-11-140-487A-1869	Sequence 1869, App

ALIGNMENTS

```
RESULT 1
US-11-297-317-21
; Sequence 21, Application US/11297317
; Publication No. US20060088525A1
; GENERAL INFORMATION:
; APPLICANT: Gregorio Avera
; APPLICANT: Frank Kolbinger
; APPLICANT: Jose M. Carballedo Herrera
; APPLICANT: Andras Aszodi
; APPLICANT: Jose W. Saldaña
; APPLICANT: Bruce M. Hall
; TITLE OF INVENTION: Therapeutic binding molecules
; FILE REFERENCE: Not Yet Known
; CURRENT APPLICATION NUMBER: US/11/297,317
; CURRENT FILING DATE: 2005-12-08
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: hypervariable region CDR3' in a CD45RO/RB binding molecule of SEQ
US-11-297-317-21
; Query Match
; Best Local Similarity 66.7%; Pred. No. 5.2e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Cy 10 QOATW 15
Db 1 QOSWTW 6

RESULT 2
US-11-140-487A-1220
; Sequence 1220, Application US/11140487A
; Publication No. US20060093617A1
; GENERAL INFORMATION:
; APPLICANT: Immunogenetics N.V.
; TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C vi.
; FILE REFERENCE: 166
; CURRENT APPLICATION NUMBER: US/11/140,487A
; CURRENT FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: EP 04012951.2
; PRIOR FILING DATE: 2004-06-01
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PRIOR APPLICATION NUMBER: EP 04447239.7
PRIOR FILING DATE: 2004-10-28
PRIOR APPLICATION NUMBER: EP 05102441.2
PRIOR FILING DATE: 2005-03-25
PRIOR APPLICATION NUMBER: US 60/576,310
PRIOR FILING DATE: 2004-06-03
PRIOR APPLICATION NUMBER: US 60/622,782
PRIOR FILING DATE: 2004-10-29
PRIOR APPLICATION NUMBER: US 60/665,395
PRIOR FILING DATE: 2005-03-25
NUMBER OF SEQ ID NOS: 2278
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1220
LENGTH: 9
TYPE: PRT
ORGANISM: hepatitis C virus
US-11-140-487A-1220

Query Match 30.6%; Score 26; DB 7; Length 9;
Best Local Similarity 80.0%; Pred. No. 5.2e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HNDSP 5
|:|:|
Db 1 HNDSP 5

RESULT 3
US-11-122-986-778
Sequence 778, Application US/11122986
Publication No. US20060104989A1
GENERAL INFORMATION:
APPLICANT: DHARMSI, ALED
APPLICANT: EDWARDS, ALED
APPLICANT: VEDADI, MASOUD
TITLE OF INVENTION: ESSENTIAL NOVEL BACTERIAL POLYPEPTIDES
FILE REFERENCE: IPT-330.01
CURRENT APPLICATION NUMBER: US/11/122,986
CURRENT FILING DATE: 2005-05-05
PRIOR APPLICATION NUMBER: 60/423,875
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: 60/423,832
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: 60/423,915
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: 60/423,757
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: 60/423,758
PRIOR FILING DATE: 2002-11-05
PRIOR APPLICATION NUMBER: 60/424,367
PRIOR FILING DATE: 2002-11-06
PRIOR APPLICATION NUMBER: 60/424,376
PRIOR FILING DATE: 2002-11-06
PRIOR APPLICATION NUMBER: 60/424,370
PRIOR FILING DATE: 2002-11-06
PRIOR APPLICATION NUMBER: 60/424,362
PRIOR FILING DATE: 2002-11-06
PRIOR APPLICATION NUMBER: 60/424,373
PRIOR FILING DATE: 2002-11-06
Remainig Prior Application data removed - See File wrapper or PALM.
NUMBER OF SEQ ID NOS: 844
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 778
LENGTH: 14
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-11-122-986-778

Query Match 29.4%; Score 25; DB 7; Length 14;
Best Local Similarity 42.9%; Pred. No. 92;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 HNDSPVR 7

Db 8 HSDTRPK 14
|:|:|:|

RESULT 4
US-10-538-066-163
Sequence 163, Application US/10538066
Publication No. US20060094649A1
GENERAL INFORMATION:
APPLICANT: EpiMune Inc.
TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen
FILE REFERENCE: 2060.015PC06
CURRENT APPLICATION NUMBER: US/10/538,066
CURRENT FILING DATE: 2005-06-09
PRIOR APPLICATION NUMBER: US 60/432,017
PRIOR FILING DATE: 2002-12-10
NUMBER OF SEQ ID NOS: 767
SOFTWARE: PatentIn version 3.2
SEQ ID NO 163
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-10-538-066-163

Query Match 27.1%; Score 23; DB 6; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 DSPVPT 8
|:|:|:|
Db 3 DSPVPT 8

RESULT 5
US-10-489-071-6
Sequence 6, Application US/10489071
Publication No. US20060094672A1
GENERAL INFORMATION:
APPLICANT: PASQUAINE ET AL.
TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF TARGETING PEPTIDES AGAINST
FILE REFERENCE: UTSC:856US
CURRENT APPLICATION NUMBER: US/10/489,071
CURRENT FILING DATE: 2004-03-08
PRIOR APPLICATION NUMBER: PCT/US02/27836
PRIOR FILING DATE: 2002-08-30
NUMBER OF SEQ ID NOS: 144
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Peptide
US-10-489-071-6

Query Match 25.9%; Score 22; DB 6; Length 7;
Best Local Similarity 80.0%; Pred. No. 5.2e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 DSPVR 7
|:|:|
Db 3 DSPVR 7

RESULT 6
US-10-546-594-92
Sequence 92, Application US/10546594
Publication No. US20060088538A1
GENERAL INFORMATION:
APPLICANT: HOSOKAWA, Saiko
APPLICANT: AOKI, Masaaki

```

; APPLICANT: HIRAKAWA, Yoko
; APPLICANT: ITRMT, Seima
; APPLICANT: UMEKI, Hiroe
; APPLICANT: SAIKAWA, Yoshiro
; APPLICANT: KUMAI, Koichiro
; APPLICANT: FUKUDA, Kazumasa
; TITLE OF INVENTION: MONOCLONAL ANTIBODY AND GENE ENCODING THE SAME, HYBRIDOMA, PHARMA
; FILE REFERENCE: 238067
; CURRENT APPLICATION NUMBER: US/10/546,594
; CURRENT FILING DATE: 2005-08-19
; PRIOR APPLICATION NUMBER: JP 2003/54670
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: JP 2003/194643
; PRIOR FILING DATE: 2003-07-09
; NUMBER OF SEQ ID NOS: 132
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 92
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-546-594-92

Query Match      25.9%: Score 22; DB 6; Length 11;
Best Local Similarity 33.3%; Pred. No. 2.4e+02;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      7 RTEQATW 15
DB      1 RASQSISSW 9
```

```

RESULT 7
US-11-140-487A-1766
; Sequence 1766, Application US/11140487A
; Publication No. US20060093617A1
; GENERAL INFORMATION:
; APPLICANT: Immunogenetics N.V.
; TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C vi
; FILE REFERENCE: 166
; CURRENT APPLICATION NUMBER: US/11/140,487A
; CURRENT FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: EP 04012951.2
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: EP 04447239.7
; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: EP 05102441.2
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/576,310
; PRIOR FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: US 60/622,782
; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US 60/665,395
; PRIOR FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2278
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1766
; LENGTH: 9
; TYPE: PRT
; ORGANISM: hepatitis C virus
; US-11-140-487A-1766
```

```

Query Match      24.7%: Score 21; DB 7; Length 9;
Best Local Similarity 57.1%; Pred. No. 5.2e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      4 SPVTEQ 10
DB      1 SPLTTNQ 7
```

```

RESULT 8
US-10-516-079-64
```

```

; Sequence 64, Application US/10516079
; Publication No. US20060088899A1
; GENERAL INFORMATION:
; APPLICANT: ALVAREZ, Vernon L.
; APPLICANT: GRIMES, Carol A.
; APPLICANT: GONDA, Matthew A.
; TITLE OF INVENTION: Combination chemotherapy with chlorotoxin
; FILE REFERENCE: 51530-5006-WO
; CURRENT APPLICATION NUMBER: US/10/516,079
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: US 60/406,033
; PRIOR FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: US 60/384,171
; PRIOR FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 64
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Pep21-SCX8_LEIGH sequence
; US-10-516-079-64

Query Match      24.7%: Score 21; DB 6; Length 10;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      8 TEQOAT 13
DB      2 TDQGMT 7
```

```

RESULT 9
US-11-023-959A-63
; Sequence 63, Application US/11023959A
; Publication No. US20060106203A1
; GENERAL INFORMATION:
; APPLICANT: Winter, Greg
; TITLE OF INVENTION: Ligand
; FILE REFERENCE: 8039/2142
; CURRENT APPLICATION NUMBER: US/11/023,959A
; CURRENT FILING DATE: 2004-12-28
; PRIOR APPLICATION NUMBER: PCT/GB03/002804
; PRIOR FILING DATE: 2003-06-30
; NUMBER OF SEQ ID NOS: 187
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 63
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-023-959A-63
```

```

Query Match      23.5%: Score 20; DB 7; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.2e+04;
Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      10 QOATW 15
DB      1 QOGARW 6
```

```

RESULT 10
US-10-981-300-34
; Sequence 34, Application US/10981300
; Publication No. US20060093599A1
; GENERAL INFORMATION:
; APPLICANT: GIORGIO, SEMALDI
; APPLICANT: GADI, GAZIT-BORNSTEIN
; TITLE OF INVENTION: ANTI-PROPERDIN ANTIBODIES, AND METHODS
; FILE REFERENCE: ABGX-005
; CURRENT APPLICATION NUMBER: US/10/981,300
```

```
; CURRENT FILING DATE: 2004-11-03
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 11
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-981-300-34
```

```
Query Match      23.5%; Score 20; DB 6; Length 11;
Best Local Similarity 33.3%; Pred. No. 5.3e+02;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      7 RTEQATTW 15
Db      1 RASQGISW 9
```

RESULT 11

```
; Sequence 84, Application US/11106014
; Publication No. US20060088846A1
; GENERAL INFORMATION:
; APPLICANT: Pagano, Michele
; APPLICANT: Chlaur, Dah Sharim
; APPLICANT: Latres, Esther
; APPLICANT: Sivasava, Promod
; APPLICANT: Chandawarkar, Rajiv
; TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT
; FILE REFERENCE: 5914-106-999
; CURRENT APPLICATION NUMBER: US/11/106,014
; CURRENT FILING DATE: 2005-04-13
; PRIOR APPLICATION NUMBER: 10/632,150
; PRIOR FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: 09/385,219
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/118,568
; PRIOR FILING DATE: 1999-02-03
; PRIOR APPLICATION NUMBER: 60/098,355
; PRIOR FILING DATE: 1998-08-28
; PRIOR APPLICATION NUMBER: 60/124,449
; PRIOR FILING DATE: 1997-03-15
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-106-014-84
```

```
Query Match      23.5%; Score 20; DB 7; Length 12;
Best Local Similarity 44.4%; Pred. No. 5.8e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      3 DSPVTEQQ 11
Db      3 EAQVRKENQ 11
```

RESULT 12

```
; Sequence 2207, Application US/11140487A
; Publication No. US20060093617A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C vi
; FILE REFERENCE: 166
; CURRENT APPLICATION NUMBER: US/11/140,487A
; CURRENT FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: EP 04012951.2
```

```
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: EP 04447239.7
; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: EP 05102441.2
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/576,310
; PRIOR FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: US 60/622,782
; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US 60/665,395
; PRIOR FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2278
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2207
; LENGTH: 15
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-11-140-487A-2207
```

```
Query Match      23.5%; Score 20; DB 7; Length 15;
Best Local Similarity 44.4%; Pred. No. 7.3e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      4 SPVTEQQA 12
Db      2 SPVFTDMS 10
```

RESULT 13

```
; Sequence 404, Application US/10538066
; Publication No. US20060094649A1
; GENERAL INFORMATION:
; APPLICANT: Epiimmune Inc.
; TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen
; FILE REFERENCE: 2060.01SPC06
; CURRENT APPLICATION NUMBER: US/10/538,066
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US 60/432,017
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 767
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 404
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-538-066-404
```

```
Query Match      22.4%; Score 19; DB 6; Length 8;
Best Local Similarity 57.1%; Pred. No. 5.2e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      9 EQQATTW 15
Db      2 EAQNTTY 8
```

RESULT 14

```
; Sequence 159, Application US/10538066
; Publication No. US20060094649A1
; GENERAL INFORMATION:
; APPLICANT: Epiimmune Inc.
; TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen
; FILE REFERENCE: 2060.01SPC06
; CURRENT APPLICATION NUMBER: US/10/538,066
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US 60/432,017
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 767
; SOFTWARE: PatentIn version 3.2
```

; SEQ ID NO 159
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-538-066-159

Query Match 22.4%; Score 19; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.2e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 QOAT 13
| | | |
| | | |
Db 1 QOAT 4

RESULT 15
US-10-538-066-429
; Sequence 429, Application US/10538066
; Publication No. US20060094649A1
; GENERAL INFORMATION:
; APPLICANT: Epiimmune Inc.
; TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen
; FILE REFERENCE: 2060.015PC06
; CURRENT APPLICATION NUMBER: US/10/538,066
; PRIOR FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US 60/432,017
; NUMBER OF SEQ ID NOS: 767
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 429
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-538-066-429

Query Match 22.4%; Score 19; DB 6; Length 9;
Best Local Similarity 57.1%; Pred. No. 5.2e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 EQOATTW 15
| | | |
| | | |
Db 2 EAQNTTY 8

Search completed: May 30, 2006, 10:25:03
Job time : 5.66667 secs

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 30, 2006, 09:58:50 ; Search time 60 Seconds
(without alignments)
114.304 Million cell updates/sec

Title: US-10-758-165A-1
Perfect score: 81
Sequence: 1 RNDSP1QTDQYTTTG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 837128

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	81	100.0	15 8 ADR10601	Adt10601 Dog IGE e
2	53	65.4	15 8 ADR10607	Adt10607 Pig IGE e
3	48	59.3	15 8 ADR10602	Adt10602 Cat IGE e
4	41	50.6	15 8 ADR10603	Adt10603 Horse IGE
5	34	42.0	15 7 ADC64568	Adc64568 Horse imm
6	32	39.5	10 5 ABG98754	ABg98754 F protein
7	32	39.5	10 5 ABG98755	ABg98755 F protein
8	32	39.5	13 2 AAR79898	Aar79898 Fusion pr
9	31	38.3	14 2 AAW35339	Aaw35339 Rat GDNF
10	31	38.3	14 2 AAW84178	Aaw84178 Rat GDNF
11	31	38.3	15 4 AEC98667	Aec98667 HLA-DR bi
12	30	37.0	14 4 AAM98177	Aam98177 Human pep
13	30	37.0	14 9 AED12588	Aed12588 Anti-Notog
14	29	35.8	10 3 AAY51451	Aay51451 AAV VP3 d
15	29	35.8	10 4 AAB46909	Aab46909 AAV mutan
16	29	35.8	10 8 ADG94454	Adg94454 Human JAM
17	29	35.8	10 8 ADI46852	Adi46852 Permeabil
18	29	35.8	10 8 ADP87029	Adp87029 Junctiona
19	29	35.8	15 8 ADR10604	Adt10604 Sheep IGE
20	28	34.6	8 7 ADJ72341	Adj72341 Streptomy
21	28	34.6	8 8 ADG94478	Adg94478 Human JAM
22	28	34.6	8 8 ADI46877	Adi46877 Permeabil
23	28	34.6	8 8 ADP87053	Adp87053 Junctiona

24	28	34.6	10 6 ABJ19566	ABj19566 Neuronal
25	28	34.6	10 8 ABY01523	ABy01523 SARS coro
26	28	34.6	10 8 ADY01210	ADy01210 SARS coro
27	28	34.6	10 9 ADZ86156	Adz86156 SARS coro
28	28	34.6	10 9 AEA45250	Aea45250 Apolipop
29	28	34.6	14 4 AAO05129	Aao05129 Peptide #
30	28	34.6	15 9 ADV51735	Adv51735 SARS-COV
31	28	34.6	15 9 ADV51737	Adv51737 SARS-COV
32	28	34.6	15 9 ADV51734	Adv51734 SARS-COV
33	28	34.6	15 9 ADV51736	Adv51736 SARS-COV
34	28	34.6	15 9 ADV51733	Adv51733 SARS-COV
35	28	34.6	15 9 ADV51739	Adv51739 SARS-COV
36	28	34.6	15 9 ADV51743	Adv51743 SARS-COV
37	28	34.6	15 9 ADV51738	Adv51738 SARS-COV
38	28	34.6	15 9 ADV51740	Adv51740 SARS-COV
39	28	34.6	15 9 ADV51741	Adv51741 SARS-COV
40	28	34.6	15 9 ADV51742	Adv51742 SARS-COV
41	27	33.3	9 9 ADW23315	Adw23315 SARS coro
42	27	33.3	9 9 ADW23210	Adw23210 SARS coro
43	27	33.3	9 9 ADW23329	Adw23329 SARS coro
44	27	33.3	9 9 AEC97896	Aec97896 HLA-A24-b
45	27	33.3	10 5 ABG98753	ABg98753 F protein

ALIGNMENTS

RESULT 1
ID ADR10601 standard; peptide; 15 AA.
AC ADR10601;
DT 21-OCT-2004 (first entry)
XX Dog IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 1.
DE
XX Antiaethmatic; Antiallergic; Immunosuppressive; IGE; dog; asthma;
KW anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody.
XX
XX Canis familiaris.
OS
XX WO2004065936-A2.
PN
XX 05-AUG-2004.
PD
XX 15-JAN-2004; 2004WO-US003566.
PF
XX 16-JAN-2003; 2003US-0440472P.
PR
XX (UYNC-) UNIV NORTH CAROLINA STATE.
PA
XX Hammerberg B;
PI
XX WPI: 2004-593545/57.
PT
XX Novel antibody that specifically binds to mammalian IGE epitope, useful
PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE
or treating asthma or anaphylactic shock.
XX
XX Example 6; Page 9; 14pp; English.
PS
XX The present invention relates to a novel monoclonal antibody (I) that
XX specifically binds to a mammalian IGE epitope, where the epitope is
XX between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
XX (I) is useful for testing an allergen reactivity of an IGE sample. The
XX allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
XX and corn allergens. The sample is a biological sample collected from a
XX dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
XX treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
XX antibodies recognise epitopes on canine IGE corresponding to amino acid
XX residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the
XX canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from

CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with
 CC either pig or human epsilon-chains of IGE.

XX Sequence 15 AA;

Query Match 100.0%; Score 81; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 5.9e-07;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RNDSPQDTQYTTTG 15
 |||||
 Db 1 RNDSPQDTQYTTTG 15

RESULT 2

ADRI0607
 ID ADRI0607 standard; peptide; 15 AA.

AC ADRI0607;

DT 21-OCT-2004 (first entry)

DE Pig IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 7.

XX Antiasthmatic; Antiallergic; Immunosuppressive; IGE; dog; asthma;
 KM anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
 XX pig.

OS Sue scrofa.

XX WO2004065936-A2.

PN 05-AUG-2004.

PD 15-JAN-2004; 2004WO-US003566.

PF 16-JAN-2003; 2003US-0440472P.

XX (UYN(-) UNIV NORTH CAROLINA STATE.

PA Hammerberg B;

PI WPI; 2004-593545/57.

DR Novel antibody that specifically binds to mammalian IGE epitope, useful
 PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE
 PT or treating asthma or anaphylactic shock.

XX Example 6; Page 9; 14pp; English.

XX The present invention relates to a novel monoclonal antibody (I) that
 CC specifically binds to a mammalian IGE epitope, where the epitope is
 CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
 CC (I) is useful for testing an allergen reactivity of an IGE sample. The
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
 CC and corn allergens. The sample is a biological sample collected from a
 CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
 CC antibodies recognise epitopes on canine IGE corresponding to amino acid
 CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the
 CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with
 CC either pig or human epsilon-chains of IGE. The present sequence is the
 CC pig IGE 5.91 recognition site.

XX Sequence 15 AA;

Query Match 65.4%; Score 53; DB 8; Length 15;
 Best Local Similarity 57.1%; Pred. No. 0.044;

Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Oy 1 RNDSPQDTQYTTT 14
 |||||
 Db 1 RNDAPVQADRHSTT 14

RESULT 3

ADRI0602
 ID ADRI0602 standard; peptide; 15 AA.

AC ADRI0602;

DT 21-OCT-2004 (first entry)

DE Cat IGE epitope recognised by monoclonal antibody 5.91, SEQ ID 2.

XX Antiasthmatic; Antiallergic; Immunosuppressive; IGE; dog; asthma;
 KM anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
 KM cat.

XX Felis catus.

XX WO2004065936-A2.

PN 05-AUG-2004.

PD 15-JAN-2004; 2004WO-US003566.

PF 16-JAN-2003; 2003US-0440472P.

XX (UYN(-) UNIV NORTH CAROLINA STATE.

PA Hammerberg B;

PI WPI; 2004-593545/57.

DR Novel antibody that specifically binds to mammalian IGE epitope, useful
 PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE
 PT or treating asthma or anaphylactic shock.

XX Example 6; Page 9; 14pp; English.

XX The present invention relates to a novel monoclonal antibody (I) that
 CC specifically binds to a mammalian IGE epitope, where the epitope is
 CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
 CC (I) is useful for testing an allergen reactivity of an IGE sample. The
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
 CC and corn allergens. The sample is a biological sample collected from a
 CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
 CC antibodies recognise epitopes on canine IGE corresponding to amino acid
 CC residues 357-371 (ADRI0601) and 146-162 (ADRI0609) respectively of the
 CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with
 CC either pig or human epsilon-chains of IGE. The present sequence is the
 CC cat IGE 5.91 recognition site.

XX Sequence 15 AA;

Query Match 59.3%; Score 48; DB 8; Length 15;
 Best Local Similarity 61.5%; Pred. No. 0.33;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 2 NDSPQDTQYTTT 14
 |||||
 Db 2 NDSPVTEQQAAT 14

RESULT 4
 ADRI0603

ID ADR10603 standard; peptide: 15 AA.
 XX
 AC ADR10603;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Horse IGE epitope recognised by monoclonal antibody 5.91. SEQ ID 3.
 XX
 KW Antiaethmatic; Antiallergic; Immunosuppressive; IGE; dog; asthma;
 KM anaphylactic shock; 5.91 monoclonal antibody; 3.76 monoclonal antibody;
 XX horse.
 XX
 OS Equus caballus.
 PN WO2004065936-A2.
 XX
 PD 05-AUG-2004.
 XX
 PF 15-JAN-2004; 2004NO-US003566.
 XX
 PR 16-JAN-2003; 2003US-0440472P.
 XX
 PA (UYNC-) UNIV NORTH CAROLINA STATE.
 XX
 PI Hammerberg B;
 XX
 DR WPI; 2004-593545/57.
 XX
 PT Novel antibody that specifically binds to mammalian IGE epitope, useful
 PT for testing an allergen reactivity of IGE sample, detecting mammalian IGE
 PT or treating asthma or anaphylactic shock.
 XX
 PS Example 6; Page 9; 14pp; English.
 XX
 CC The present invention relates to a novel monoclonal antibody (I) that
 CC specifically binds to a mammalian IGE epitope, where the epitope is
 CC between amino acids 145-166 or 356-374 of mammalian IGE, e.g. dog IGE.
 CC (I) is useful for testing an allergen reactivity of an IGE sample. The
 CC allergen is chosen from mold, pollen, dust mite, milk, egg, soy, peanut
 CC and corn allergens. The sample is a biological sample collected from a
 CC dog, cat or horse. (I) is also useful for detecting mammalian IGE and for
 CC treating asthma or anaphylactic shock. The 5.91 and 3.76 monoclonal
 CC antibodies recognise epitopes on canine IGE corresponding to amino acid
 CC residues 357-371 (ADR10601) and 146-162 (ADR10609) respectively of the
 CC canine IGE epsilon-chain. Recognition of epsilon-chains from IGE from
 CC cat, horse, pig and human by 5.91 and 3.76 was examined. Both 5.91 and
 CC 3.76 were observed to have good cross-reactivity with the epsilon-chain
 CC of IGE from cat and horse, but did not exhibit cross-reactivity with
 CC either pig or human epsilon-chains of IGE. The present sequence is the
 CC horse IGE 5.91 recognition site.
 XX
 SQ Sequence 15 AA;
 XX
 Query Match 50.6%; Score 41; DB 8; Length 15;
 Best Local Similarity 64.3%; Pred. No. 5.4;
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 Qy 1 RNDSPIDQDYTTT 14
 ||: ||||| ||
 Db 1 RNNVLIQDQOATT 14
 ||: ||||| ||
 RESULT 5
 ID ADC64568 standard; peptide: 15 AA.
 XX
 AC ADC64568;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Horse immunoglobulin E, IGE, heavy chain immunogenic peptide P4.
 XX
 KW Horse; immunoglobulin E, IGE; heavy chain; immunogen; allergy.

XX
 OS Equus caballus.
 XX
 PN US2003087314-A1.
 XX
 DT 08-MAY-2003.
 XX
 DE 08-NOV-2001; 2001US-00052788.
 XX
 PR 08-NOV-2001; 2001US-00052788.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Gershwin LJ, Pettigrew HD, Kalina WV;
 XX
 DR WPI; 2003-765437/72.
 XX
 PT Immunogenic composition comprising an isolated equine immunoglobulin E
 PT polypeptide that induces production of antibodies which specifically bind
 PT to equine immunoglobulin E.
 XX
 PS Example 1; Page 8; 14pp; English.
 XX
 CC The invention relates to an immunogenic composition comprising an
 CC isolated polypeptide having an amino acid sequence that is at least 80%
 CC identical to 6 (S1-S6), amino acid peptide sequences derived from
 CC equine immunoglobulin E (the composition induces production of an
 CC antibody that specifically binds to equine immunoglobulin (Ig)E, the six
 CC polypeptides are not explicitly identified in the specification. Also
 CC included are a composition comprising an antibody that specifically binds
 CC to a polypeptide at least 80% identical to (S1)-(S6), an antibody that
 CC specifically binds to equine IGE made by the process of immunising an
 CC animal with a polypeptide at least 80% identical to (S1)-(S6), making an
 CC antibody that specifically binds to equine IGE (involving immunising an
 CC animal with a composition further comprising an isolated polypeptide (the
 CC amino acid sequence of the polypeptide is at least 80% identical to (S1)-
 CC (S6)), and collecting antiserum from the animal) and a kit for detection
 CC of equine IGE in a biological sample comprising the antibody and means
 CC for detecting specific binding of the antibody to equine IGE. The
 CC antibody is useful for detecting equine IGE protein in a biological
 CC sample (serum) which involves contacting the sample with the presence or
 CC absence of an antigen/antibody complex, and detecting the presence or
 CC absence of the antigen/antibody complex. The antibody and antigen are
 CC immobilised on a solid surface. The antibody is labelled such that the
 CC complex can be detected. The complex is detected using a second labelled
 CC antibody. The peptides are useful for generating antibodies specific for
 CC IGE which can serve as a diagnostic test for allergy. The present
 CC sequence is a Horse immunoglobulin E, IGE, heavy chain immunogenic
 CC peptide from the early portion of the C4 region.
 XX
 SQ Sequence 15 AA;
 XX
 Query Match 42.0%; Score 34; DB 7; Length 15;
 Best Local Similarity 77.8%; Pred. No. 89;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 6 IQDQYTTT 14
 ||||| ||
 Db 1 IQDQOATT 9
 ||||| ||
 RESULT 6
 ID ABG98754 standard; peptide: 10 AA.
 XX
 AC ABG98754;
 XX
 DT 13-JAN-2003 (first entry)
 XX
 DE F protein decapeptide #241.
 XX
 KW F protein; RSV; decapeptide; negative sense single stranded RNA virus;
 KW viral F protein; F protein mediated host cell virion fusion; virucide;

KW F protein mediated host cell virion budding.
 XX
 OS Respiratory syncytial virus.
 XX
 PN WO200242326-A1.
 XX
 PD 30-MAY-2002.
 XX
 XX
 PE 22-NOV-2001; 2001WO-AU001517.
 XX
 PR 22-NOV-2000; 2000US-0252767P.
 XX
 PA (BIOT-) BIOTA SCI MANAGEMENT PTY LTD.
 XX
 PI Mason AJ, Tucker SP, Young PR;
 XX
 DR WPI; 2002-599372/64.
 XX
 PT Facilitating production of a protein for analyzing, designing and/or
 PT modifying an agent that can interact with a viral F protein, comprises
 PT expressing a nucleic acid optimized for expression of the protein, using
 PT a eukaryotic cell.
 XX
 PS Claim 42; Page 102; 367pp; English.

The invention relates to a method for facilitating production of a protein or its derivative from a negative sense single stranded RNA virus, by expressing a nucleic acid molecule encoding the protein in a host cell, where the nucleic acid is optimised for expression by a eukaryotic cell. The protein, especially F protein, is useful for analysing, designing and/or modifying an agent capable of interacting with a viral F protein or its derivative and modulating a functional activity associated with the protein, by contacting the protein with a putative agent and assessing the degree of interactive complementarity of the agent with the protein. An optimised nucleic acid or its derivative, equivalent, analogue or mimetic is useful for interacting with a viral F protein and modulating a functional activity associated with the viral protein, for use in the manufacture of a medicament utilised in the therapeutic and/or prophylactic treatment of conditions characterised by infection with a negative sense single stranded RNA virus, and for modulating a functional activity associated with a viral F protein in a subject, preferably a mammal, especially a human, where the functional activity is F protein mediated host cell virion fusion and/or virion budding and the modulating is down regulation. Sequences ABG96514-ABG95058 represent F protein decapitides of the invention

Sequence 10 AA:

Query Match	39.5%	Score 32;	DB 5;	Length 10;
Best Local Similarity	66.7%;	Pred. No. 1.3e+02;		
Matches 6; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

QY 2 NDSPITDQ 10
|||
Db 2 NDMPTNDQ 10

RESULT 7
ABG98755
ID ABG98755 standard; peptide: 10 AA.

AC ABG98755;

DT 13-JAN-2003 (first entry)

DE F protein decapeptide #242.

KW F protein; RSV, decapeptide; negative sense single stranded RNA virus;

KW F protein mediated host cell virion budding.

OS Respiratory syncytial virus.

XX

PN WO000242326-A1.
XX
XX 30-MAY-2002.
XX
XX 22-NOV-2001; 2001WO-AU001517.
XX
XX 22-NOV-2000; 2000US-0252767P.
XX
XX (BIOT-) BIOTA SCI MANAGEMENT PTY LTD.
PA
XX
XX
PI Mason AJ, Tucker SP, Young PR;
XX MPI; 2002-599372/64.
XX
XX
PT Facilitating production of a protein for analyzing designing and/or
PT modifying an agent that can interact with a viral P protein, comprises
PT expressing a nucleic acid optimized for expression of the protein, using
PT a eukaryotic cell.
XX
XX Claim 42; Page 102; 367pp; English.

CC The invention relates to a method for facilitating production of a
 CC protein or its derivative from a negative sense single stranded RNA
 CC virus, by expressing a nucleic acid molecule encoding the protein in a
 CC host cell, where the nucleic acid is optimised for expression by a
 CC eukaryotic cell. The protein, especially F protein, is useful for
 CC analysing, designing and/or modifying an agent capable of interacting
 CC with a viral F protein or its derivative and modulating a functional
 CC activity associated with the protein, by contacting the protein with a
 CC putative agent and assessing the degree of interactive complementarity of
 CC the agent with the protein. An optimised nucleic acid or its derivative,
 CC equivalent, analogue or mimetic is useful for interacting with a viral F
 CC protein and modulating a functional activity associated with the viral
 CC protein, for use in the manufacture of a medicament utilised in the
 CC therapeutic and/or prophylactic treatment of conditions characterised by
 CC infection with a negative sense single stranded RNA virus, and for
 CC modulating a functional activity associated with a viral F protein in a
 CC subject, preferably a mammal, especially a human, where the functional
 CC activity is F protein mediated host cell vitron function and/or virion
 CC budding and the modulating is down regulation. Sequences ABG38514-
 CC ABG39058 represent F protein decapetptides of the invention
 XX

Query Match	39.5%	Score 32;	DB 5;	Length 10;
Best Local Similarity	66.7%	Pred. No. 1.3e+02;		
Matches 6; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

QY 2 NDSPIQTDD 10
|||
Db 1 NDMPIITNDQ 9

RESULT 8
AAR79898
ID AAR79898 standard; peptide: 13 AA.

AC AAR79898;

DT 25-MAR-2003 (revised)

XX

XX XX

KW human; therapy; diagnosis; immunoassay.

OS Synthetic.

CA1336955-C.
PN
XY

PD 12-SEP-1995.
XX

XX

PF 20-SEP-1989; 89CA-00612131.
XX 20-SEP-1988; 88US-00247017.
PR 20-SEP-1989; 89US-00409915.
XX
XX (PRAXIS-) PRAXIS BIOLOGICS INC.
XX
XX Paradoiso PR, Hu BT, Arumugham R, Hildreth SW, Martin-Gallardo A,
PI Welsh EE;
DR WPI; 1995-328674/43.
XX
PT Sub-unit vaccine against respiratory syncytial virus - contains
PT polypeptide related to neutralising epitope on G protein, opt. also
PT polypeptide from F protein.
XX
XX Disclosure; Fig 3; 11pp; English.
XX
CC The sequences represented by AAR79895-R79899 are synthetic peptides
CC corresponding to regions of the respiratory syncytial (RS) virus fusion
CC protein (see AAR79894). This sequence corresponds to residues 261-273.
CC These fragments were used to create antibodies. The DNA encoding these
CC fragments is inserted into expression vectors and used to transform cell
CC cultures, the expressed protein is then isolated and purified. These
CC peptide fragments are then used in a vaccine. Alternatively, the
CC antibodies against these fragments could be used to confer short-term
CC protection against the RS virus. The vaccine can then be used to protect
CC humans and animals (for animals, the RS sequence used is from the RS
CC virus of that species). The dose of the vaccine is 0.1-100 micro grammes
CC per kg body weight. The vaccine can also be used in diagnosis, such as
CC immunoassays. The DNA encoding this sequence can be used in hybridisation
CC tests to detect RS virus in blood. The antibodies can be used to identify
CC viral epitopes. The advantage with using this methodology is that there
CC is no enhancement/potentiation of the disease seen with current
CC treatments. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 13 AA:
Query Match 39.5%; Score 32; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 NDSPIQTDQ 10
Db 2 NDMPTINDQ 10
RESULT 9
AAM5339
ID AAM35339 standard; peptide; 14 AA.
XX
XX AAM35339;
AC
XX
XX 01-MAY-1998 (first entry)
DT
XX
XX Rat GDNF receptor residues 356-369.
DE
XX
XX Rat; glial cell line-derived neurotrophic factor; GDNF; receptor;
XX treatment; dopaminergic nerve cell disorder; Parkinson's disease;
XX Alzheimer's disease; amyotrophic lateral sclerosis; diabetes;
XX Huntington's disease; glaucoma; retinal degeneration; hearing loss;
XX gene therapy.
XX
XX Rattus sp.
OS
XX
XX W09740152-A1.
PN
XX
XX 30-OCT-1997.
PD
XX
XX 15-APR-1997; 97WO-US006281.
PF
XX
XX 22-APR-1996; 96US-0015907P.
PR
XX
XX 09-MAY-1996; 96US-0017221P.
PR

BR 14-APR-1997; 97US-00837199.
XX
XX (AMGEN-) AMGEN INC.
PA
XX
XX Fox GM, Wen D, Jing S;
PI
XX
XX WPI; 1997-535836/49.
DR
XX
XX Glial cell line derived neurotrophic factor receptor - useful to treat
PT dopaminergic nerve cell disorders, e.g. Parkinson's and Alzheimer's
PT disease.
PT
XX
XX Disclosure; Page 21; 19pp; English.
XX
XX The present peptide is derived from rat glial cell line-derived
CC neurotrophic factor (GDNF) receptor, which can be used to treat
CC dopaminergic nerve cell disorders, e.g. Parkinson's and Alzheimer's
CC disease or amyotrophic lateral sclerosis, complications of diabetes and
CC Huntington's disease and (optionally in combination with GDNF) glaucoma,
CC retinal degeneration and hearing loss caused by injury to inner ear
CC sensory neurons. The receptor can also be used to block unwanted GDNF
CC activity, analyse GDNF related molecules and stabilise GDNF in
CC pharmaceutical formulations. Receptor expressing cells, preferably
CC transfected ex vivo, can be used similarly by implantation, and the use
CC of the receptor cDNA in gene therapy is also contemplated. Probes based
CC on the cDNA can be used to identify GDNF responsive cells and tissues,
CC e.g. to identify patients who would benefit from GDNF therapy, and
CC abnormalities in receptor expression, and to isolate molecules that form
CC a complex with the cDNA or are homologous/cross-reactive with the cDNA.
CC Anti-receptor antibodies, oligonucleotides derived from the cDNA and
CC animal models that overexpress the receptor can be used to study the
CC biological function of GDNF, knockout transgenic animals can be used to
CC detect GDNF dependent neurons or processes and the antibody can be used
CC in immunoassays for the receptor. The receptor binds GDNF specifically
CC and with high affinity, acting as part of a complex that
CC mediates/enhances signal transduction by GDNF, i.e. increasing dopamine
CC uptake in dopaminergic cells
XX
SQ Sequence 14 AA:
Query Match 38.3%; Score 31; DB 2; Length 14;
Best Local Similarity 60.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 5 PIQTDQYTTT 14
Db 4 PVQTTRATTT 13
RESULT 10
AAM84178
ID AAM84178 standard; peptide; 14 AA.
XX
XX AAM84178;
AC
XX
XX 25-MAR-1999 (first entry)
DT
XX
XX Rat GDNFR-alpha derived peptide.
DE
XX
XX Rat; glial cell line derived neurotrophic factor receptor-alpha;
XX GDNFR-alpha; glial cell line-derived neurotrophic factor; GDNF;
XX neurotrophin; signal transduction; dopaminergic nerve cell;
XX Parkinson's disease; Alzheimer's disease; amyotrophic lateral sclerosis;
XX neurological disorder; diabetes; glaucoma; sensory neuron;
XX retinal ganglion cell degeneration; sensory neuropathy; retinopathy;
XX gene therapy.
XX
XX Synthetic.
OS
XX
XX Rattus sp.
PN
XX
XX W09854213-A2.
PD
XX
XX 03-DEC-1998.
PD

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XX 27-APR-1998; 98WO-US008486.
XX
XX 30-MAY-1997; 97US-00866354.
XX
XX (AMGE-) AMGEN INC.
XX
XX Fox GM, Jing S, Wen D,
XX
XX WPI; 1999-080806/07.
XX
XX New isolated glial cell line-derived neurotrophic factor receptors - used
XX to develop products for treating e.g. improperly functioning dopaminergic
XX nerve cells, Parkinson's disease, Alzheimer's disease or amyotrophic
XX lateral sclerosis.
XX
XX Disclosure; Page 24; 318pp; English.
XX
XX The present peptide is derived from rat glial cell line derived
XX neurotrophic factor receptor-alpha (GDNFR-alpha) amino acids 356-369. It
XX is used to raise antibodies against GDNFR-alpha. The peptide may also
XX possess an activity of GDNFR-alpha. The GDNFR-alpha protein is capable of
XX complexing with glial cell line-derived neurotrophic factor (GDNF) and
XX mediating cell response to GDNF. GDNFR-alpha proteins are functionally
XX characterised by the ability to bind GDNF and/or neuritin specifically,
XX and to act as part of a molecular complex which mediates or enhances the
XX signal transduction affects of GDNF and/or neuritin. The proteins can be
XX used for treating improperly functioning dopaminergic nerve cells,
XX Parkinson's disease, Alzheimer's disease or amyotrophic lateral
XX sclerosis. They can also be used for treating neurological disorders
XX associated with diabetes, glaucoma or other diseases and conditions
XX involving retinal ganglion cell degeneration, sensory neuropathy caused
XX by injury to, insults to, or degeneration of, sensory neurons,
XX pathological conditions, or disease or injury-related retinopathies. The
XX products can also be used for detection, diagnosis, drug screening and
XX gene therapy
XX
XX Sequence 14 AA;
XX
XX Query Match 38.3%; Score 31; DB 2; Length 14;
XX Best Local Similarity 60.0%; Pred. No. 2.8e+02;
XX Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
XX
XX 5 PIOTDQYTTT 14
XX |:|||
XX 4 PVQTTTATT 13
XX
XX RESULT 11
XX AEC98667
XX ID AEC98667 standard; peptide; 15 AA.
XX
XX AEC98667;
XX
XX 01-DEC-2005 (first entry)
XX
XX HLA-DR binding epitope from HPV E2 protein #156.
XX
XX Human papilloma virus infection; virucide; cancer; cytostatic; vaccine;
XX epitope mapping; immune stimulation; cytotoxic T-lymphocyte;
XX human leukocyte antigen.
XX
XX Human papillomavirus.
XX
XX WO2005089164-A2.
XX
XX 29-SEP-2005.
XX
XX 03-JAN-2005; 2005WO-US000077.
XX
XX 31-DEC-2003; 2003US-0533211P.
XX
XX 02-JUL-2004; 2004US-0584652P.
XX

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PA (EPIM-) EPIMUNE INC.
PA (INNO-) INNOGENETICS NV.
PA (CHES/) CHESNUT R.
PA (NEMW/) NEWMAN M J.
PA (MOTH/) MOTH E.
PA (BAKE/) BAKER D.
PA (SOUT/) SOUTHOOD S.
PA (BABE/) BABE L M.
PA (CHEN/) CHEN Y.
PA (DEYO/) DEYOUNG L M.
PA (HUAN/) HUANG M T F.
PA (POME/) POWER S D.
PI Chesnut R, Newman MJ, Mothe B, Baker D, Southwood S, Babe LM;
PI Chen Y, Deyoung LM, Huang MTF, Power SD;
XX
XX WPI; 2005-658982/67.
XX
XX New polynucleotide comprises a multi-epitope construct comprising nucleic
XX acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte
XX (CTL) epitopes, useful in preparing a vaccine against HPV.
XX
XX Disclosure; Page 333; 518pp; English.
XX
XX The invention relates to a new polynucleotide comprising a multi-epitope
XX construct comprising nucleic acids encoding the human papillomavirus
XX (HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16 E1, E2, E4, and E7
XX are directly or indirectly joined to one another in the same reading
XX frame, a vaccine multigene. Also included are a vector comprising the
XX multi-epitope construct, a polypeptide comprising an amino acid sequence
XX encoded by the polynucleotide, a composition (comprising the
XX polynucleotide, vector and/or polypeptide and a carrier), a cell
XX (comprising the polynucleotide, vector or polypeptide), inducing an
XX immune response against human papillomavirus virus (HPV), and making the
XX polynucleotide, vector or polypeptide. The epitopes are derived from
XX different strains of HPV and are from the E1, E2, E6 and E7 proteins. The
XX epitopes may be linked via a GP-anchor/spacer peptide. The order of the
XX epitopes in the vaccine protein are disclosed in the tables referred to
XX in the claims of the specification. The polynucleotide, vector or
XX polypeptide is useful in preparing a composition for inducing an immune
XX response against human papillomavirus virus (HPV) and thus providing a
XX defense against HPV infection and HPV-related cancers. The present
XX sequence is an HPV-derived peptide epitope that binds to a subclass of
XX human leukocyte antigen (HLA) peptides.
XX
XX Sequence 15 AA;
XX
XX Query Match 38.3%; Score 31; DB 9; Length 15;
XX Best Local Similarity 55.6%; Pred. No. 3e+02;
XX Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
XX
XX 4 SPIOTDQYT 12
XX |:||:|
XX 2 SPYRTDEMT 10
XX
XX Db
XX
XX RESULT 12
XX AAM98177
XX ID AAM98177 standard; peptide; 14 AA.
XX
XX AAM98177;
XX
XX 24-JAN-2002 (first entry)
XX
XX Human peptide #1452 encoded by a SNP oligonucleotide.
XX
XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
XX neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
XX amyloid protein; angiopoietin; apoptosis related protein; cadherin;
XX cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
XX complement related protein; cytochrome; kinesin; cytokine; interferon;
XX interleukin; G-protein coupled receptor; thioesterase; inflammation;
XX multifactorial disease; autoimmune disease; infection;
XX

```

KM nervous system disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200147944-A2.
 XX
 PD 05-JUL-2001.
 XX
 PF 28-DEC-2000; 2000WO-US035498.
 XX
 PR 28-DEC-1999; 99US-0173419P.
 PR 27-DEC-2000; 2000US-00173419.
 XX
 PA (CURA-) CURAGEN CORP.
 PI Shinkets RA, Leach M;
 DR WPI; 2001-465210/50.
 XX
 PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
 PT autoimmune diseases and infections.
 XX
 PS Disclosure; Page 3986; 4143pp; English.
 XX
 CC The present invention relates to oligonucleotides (see AAL26793-AAL34659)
 CC encoding polymorphic variants of proteins related to amylases, amyloid
 CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
 CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
 CC complement related proteins, cytochromes, kinesins, cytokines,
 CC interferons, interleukins, G-protein coupled receptors and thioesterases.
 CC The present sequence is a peptide encoded by one such oligonucleotide.
 CC The oligonucleotides and the peptides encoded by them may be used in the
 CC prevention, diagnosis and treatment of diseases associated with
 CC inappropriate expression of the proteins listed above. Disorders that may
 CC be prevented, diagnosed and/or treated include multifactorial diseases
 CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
 CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
 CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
 CC brain, breast, colon and kidney, leukemia), diseases of the nervous
 CC system and an infection of pathogenic organisms
 CC
 SQ Sequence 14 AA;
 Query Match 37.0%; Score 30; DB 4; Length 14;
 Best Local Similarity 55.6%; Pred. No. 4.1e+02;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 Oy 6 IQTQDYTTT 14
 :|||:|:
 Db 5 VQTDKVTST 13
 RESULT 13
 AED12588
 ID AED12588 standard; peptide: 14 AA.
 XX
 AC AED12588;
 XX
 DT 01-DEC-2005 (first entry)
 XX
 DE Anti-Nogor scFv protein NCF0121 HC CDR3 sequence.
 XX
 KM Neuroprotective; Vulnerary; Vasotropic; Cerebroprotective;
 KM spinal cord injury; brain injury; paralysis; neurodegenerative disease;
 KM cerebrovascular ischemia; Nogo receptor; Nogor.
 XX
 OS Homo sapiens.
 XX
 PN US2005215770-A1.
 XX
 PD 29-SEP-2005.
 XX

PF 25-MAR-2005; 2005US-00090847.
 XX
 PR 26-MAR-2004; 2004US-0556386P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Bell A, Rosen CA;
 DR WPI; 2005-648835/66.
 XX
 PT New antibody or its fragment that specifically binds Nogo receptor
 PT (Nogor), useful in preparing a composition for treating or ameliorating
 PT spinal cord injury, brain trauma, paralysis, neurodegenerative disorders
 PT or stroke.
 XX
 PS Example 1; Page 69; 81pp; English.
 XX
 CC The present invention relates to a novel antibody or its fragment (e.g.
 CC an scFv) that binds to the Nogo receptor (Nogor; AED12284). The antibody
 CC comprises a Variable Heavy Complementarity Determining Region (VHCDR1),
 CC VHCDR2 or VHCDR3 and a Variable Light Complementarity Determining Region
 CC (VLCDR1, VLCDR2 or VLCDR3). The antibody prevents binding or inhibits
 CC interaction of Nogor with: p75 (NTR) (AED12288); LINGO-1 (AED12289); Nogo
 CC (AED12285); OMgp (AED12286); or MAG (AED12287), and promotes neurite
 CC outgrowth or axonal regeneration. The antibody is useful in preparing a
 CC composition for treating or ameliorating spinal cord injury, brain
 CC trauma, paralysis, neurodegenerative disorders or stroke. The present
 CC sequence is a CDR peptide sequence for one such scFv that binds to Nogor.
 SQ Sequence 14 AA;
 Query Match 37.0%; Score 30; DB 9; Length 14;
 Best Local Similarity 45.5%; Pred. No. 4.1e+02;
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 Oy 5 PIQTQDYTTT 15
 :|||:|:
 Db 1 PLSDYDTSG 11
 RESULT 14
 AAY51451
 ID AAY51451 standard; peptide: 10 AA.
 XX
 AC AAY51451;
 XX
 DT 11-MAY-2000 (first entry)
 XX
 DE AAV VP3 derived peptide fragment #6.
 XX
 KM VP3; structural protein; capsid; tropism; diagnosis; gene therapy.
 XX
 OS Adeno-associated virus.
 XX
 PN WO9967393-A2.
 XX
 PD 29-DEC-1999.
 XX
 PF 21-JUN-1999; 99WO-EP004288.
 XX
 PR 19-JUN-1998; 98DE-01027457.
 XX
 PA (MEDI-) MEDIGENE AG.
 PI Hallek M, Ried M, Deleage G, Girod A;
 DR WPI; 2000-160586/14.
 XX
 PT Structure proteins of adeno-associated virus with at least one mutation
 PT have increased infectiveness.
 XX
 PS Example 2; Page 42; 43pp; German.
 XX

CC This invention describes novel structural proteins of adeno-associated
CC virus (AAV) especially AAV-capsids with at least one mutation and which
CC have an increased infectiveness. The structural proteins are used to
CC alter the tropism of AAV, to transform cells, for diagnosis and for
CC effectively studies for gene therapy and/or for genomic targeting.
CC AAV51446-Y51467 represent AAV derived peptides used to illustrate the
CC method of the invention

XX
SQ Sequence 10 AA;

Query Match 35.8%; Score 29; DB 3; Length 10;
Best Local Similarity 50.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 4 SPIQTDQY 11
: : : : :
Db 1 NPVATEQY 8

RESULT 15

AAB46909
ID AAB46909 standard; peptide; 10 AA.

XX
AC AAB46909;

XX
DT 04-MAY-2001 (first entry)

XX
DE AAV mutant VP3 derived peptide SEQ ID 14.

XX
KW VP3 protein; structural protein; chromatography; tropism; antigenicity;
XX genomic targeting; gene therapy; purification; affinity tag.

XX
OS Adeno associated virus.

XX
PN DE19933719-A1.

XX
PD 25-JAN-2001.

XX
PF 19-JUL-1999; 99DE-01033719.

XX
PR 19-JUL-1999; 99DE-01033719.

XX
PA (MEDI-) MEDIGENE AG.

XX
PI Hallek M, Girod A, Ried M, Koerner C;

XX
DR WPI; 2001-203661/21.

XX
PT New mutant adeno-associated virus structural protein with altered
XX chromatographic properties, useful in preparation of gene therapy
XX vectors.

XX
PS Example 1; Page 15; 20pp; German.

XX
CC This invention describes a novel structural protein (I) of adeno-
CC associated virus (AAV) which has at least one mutation that alters the
CC chromatographic properties of the virus. The invention also describes (1)
CC a nucleic acid (II) that encodes (I); (2) a cell (III) containing (II);
CC and (3) producing (I) comprising culturing (III). (I), (II) and (III) are
CC used to purify AAV and its particles, to alter the tropism or
CC antigenicity of AAV, to transform cells, for genomic targeting, for
CC diagnosis, for examination of activity and/or gene therapy. Altering the
CC chromatographic properties improves purification, especially
CC concentration of virus and produces viral particles to a higher titre or
CC higher purity and/or provides more efficient purification (fewer steps,
CC and a quicker and less expensive process). Particularly, mutated (I)
CC result in viruses that are eluted at a different (higher or lower) salt
CC concentration than the wild type, which tends to co-elute with other
CC viruses, serum proteins and cellular debris, or that include a specific
CC affinity tag. Mutation may also allow targeting of cells, e.g.
CC hematopoietic cells, that are not normally targets for AAV

XX
SQ Sequence 10 AA;

Query Match 35.8%; Score 29; DB 4; Length 10;
Best Local Similarity 50.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 4 SPIQTDQY 11
: : : : :
Db 1 NPVATEQY 8

Search completed: May 30, 2006, 10:12:43
Job time : 61 secs

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OM protein - protein search, using sw model

Run on: May 30, 2006, 10:21:55 ; Search time 47 Seconds

(without alignments)
147.835 Million cell updates/sec

Title: US-10-758-165A-1

Sequence: 1 RNDSPIDQDTTGTG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 395127

Minimum DB seq length: 0
Maximum DB seq length: 15Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:

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1: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubppaa/US11_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	100.0	15	5	US-10-758-165-1
2	53	65.4	15	5	US-10-758-165-7
3	48	59.3	15	5	US-10-758-165-2
4	41	50.6	15	5	US-10-758-165-3
5	34	42.0	15	4	US-10-052-788-4
6	32	39.5	10	4	US-10-432-234A-249
7	32	39.5	10	4	US-10-432-234A-250
8	31	38.3	14	4	US-10-155-693-29
9	31	38.3	14	5	US-10-872-161-29
10	29	35.8	10	4	US-10-462-452-433
11	29	35.8	10	4	US-10-601-953-561
12	29	35.8	10	4	US-10-322-266-434
13	29	35.8	12	3	US-09-990-832C-108
14	29	35.8	15	5	US-10-758-165-4
15	28	34.6	8	4	US-10-462-452-457
16	28	34.6	8	4	US-10-601-953-586
17	28	34.6	8	4	US-10-322-266-458
18	28	34.6	10	5	US-10-475-049A-24
19	28	34.6	10	5	US-10-936-237-18
20	28	34.6	11	4	US-10-378-173-28
21	27	33.3	10	4	US-10-281-479A-27
22	27	33.3	10	4	US-10-275-180A-27
23	27	33.3	10	4	US-10-286-132A-27
24	27	33.3	10	4	US-10-432-234A-248
25	27	33.3	13	5	US-10-948-707-846
26	27	33.3	13	5	US-10-948-707-949
27	27	33.3	15	4	US-10-080-608A-161

28	27	33.3	15	4	US-10-370-485-70	Sequence 70, Appl
29	26	32.1	9	4	US-10-428-135-103	Sequence 103, App
30	26	32.1	10	3	US-09-572-404B-1728	Sequence 1728, Ap
31	26	32.1	10	4	US-10-149-138-543	Sequence 543, App
32	26	32.1	10	4	US-10-149-138-1265	Sequence 1265, Ap
33	26	32.1	10	4	US-10-149-138-1902	Sequence 1902, Ap
34	26	32.1	10	4	US-10-149-138-543	Sequence 543, App
35	26	32.1	10	4	US-10-149-138-1265	Sequence 1265, Ap
36	26	32.1	10	4	US-10-149-138-1902	Sequence 1902, Ap
37	26	32.1	10	4	US-10-432-234A-251	Sequence 251, App
38	26	32.1	10	5	US-10-475-049A-15	Sequence 15, Appl
39	26	32.1	12	4	US-10-078-968-5	Sequence 5, Appl1
40	26	32.1	12	4	US-10-279-991-13	Sequence 13, Appl
41	26	32.1	13	5	US-10-948-707-1324	Sequence 1324, Ap
42	26	32.1	14	3	US-09-826-230-126	Sequence 126, App
43	26	32.1	14	4	US-10-264-309-71	Sequence 71, Appl
44	26	32.1	14	5	US-10-264-309-71	Sequence 2185, Ap
45	26	32.1	14	5	US-10-530-061-2185	

ALIGNMENTS

```
RESULT 1
US-10-758-165-1
; Sequence 1, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammeberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Canis familiaris
US-10-758-165-1

Query Match      100.0%   Score 81;   DB 5;   Length 15;
Best Local Similarity 100.0%   Pred. No. 5; 4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  RNDSPIDQDTTGTG 15
Db      1  RNDSPIDQDTTGTG 15

RESULT 2
US-10-758-165-7
; Sequence 7, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammeberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Sus scrofa
US-10-758-165-7

Query Match      65.4%   Score 53;   DB 5;   Length 15;
```

Best Local Similarity 57.1%; Pred. No. 0.039; DB 5; Length 15;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 RNDSPQTDQYTTT 14
|||:|:|:|:|
Db 1 RNDAPVQADHRSTT 14

RESULT 3

US-10-758-165-2
; Sequence 2, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:

APPLICANT: Hamnerberg, Bruce
TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
FILE REFERENCE: 5051-661
CURRENT APPLICATION NUMBER: US/10/758,165
CURRENT FILING DATE: 2004-01-16
PRIOR APPLICATION NUMBER: US 60/440,472
PRIOR FILING DATE: 2003-01-16
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 15
TYPE: PRT
ORGANISM: Felis catus

US-10-758-165-2

Query Match 59.3%; Score 48; DB 5; Length 15;
Best Local Similarity 61.5%; Pred. No. 0.29;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPIQTDQYTTT 14
|||:|:|:|:|
Db 2 NDSPIQTDQYTTT 14

RESULT 4

US-10-758-165-3
; Sequence 3, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:

APPLICANT: Hamnerberg, Bruce
TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
FILE REFERENCE: 5051-661
CURRENT APPLICATION NUMBER: US/10/758,165
CURRENT FILING DATE: 2004-01-16
PRIOR APPLICATION NUMBER: US 60/440,472
PRIOR FILING DATE: 2003-01-16
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3
LENGTH: 15
TYPE: PRT
ORGANISM: Equus caballus

US-10-758-165-3

Query Match 50.6%; Score 41; DB 5; Length 15;
Best Local Similarity 64.3%; Pred. No. 4.7;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 RNDSPQTDQYTTT 14
|||:|:|:|:|
Db 1 RNDAPVQADHRSTT 14

RESULT 5

US-10-052-788-4
; Sequence 4, Application US/10052788
; Publication No. US20030087314A1
; GENERAL INFORMATION:

APPLICANT: Gerishwin, Laurel J.
APPLICANT: Pettigrew, Howard David

APPLICANT: Kalina, Warren V.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Epsilon Immunoglobulin Chain Derived Peptides for

FILE REFERENCE: 023070-121000US
CURRENT APPLICATION NUMBER: US/10/052,788
CURRENT FILING DATE: 2001-11-08
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: epitope peptide
OTHER INFORMATION: P4, early portion of C4 of equine IgE epsilon
US-10-052-788-4

Query Match 42.0%; Score 34; DB 4; Length 15;
Best Local Similarity 77.8%; Pred. No. 76;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 IQTDQYTTT 14
|||:|:|:|:|
Db 1 IQTDQYTTT 9

RESULT 6

US-10-432-234A-249
; Sequence 249, Application US/10432234A
; Publication No. US20040161846A1
; GENERAL INFORMATION:

APPLICANT: Biocr Scientific Management Pty Ltd
TITLE OF INVENTION: A method of expression and agents identified thereby
FILE REFERENCE: 12084720/TDO
CURRENT APPLICATION NUMBER: US/10/432,234A
CURRENT FILING DATE: 2003-05-22
PRIOR APPLICATION NUMBER: US 60/252767
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 574
SOFTWARE: PatentIn version 3.1
SEQ ID NO 249
LENGTH: 10
TYPE: PRT
ORGANISM: respiratory syncytial virus

US-10-432-234A-249

Query Match 39.5%; Score 32; DB 4; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 NDSPIQTDQ 10
|||:|:|:|:|
Db 2 NDSPIQTDQ 10

RESULT 7

US-10-432-234A-250
; Sequence 250, Application US/10432234A
; Publication No. US20040161846A1
; GENERAL INFORMATION:

APPLICANT: Biocr Scientific Management Pty Ltd
TITLE OF INVENTION: A method of expression and agents identified thereby
FILE REFERENCE: 12084720/TDO
CURRENT APPLICATION NUMBER: US/10/432,234A
CURRENT FILING DATE: 2003-05-22
PRIOR APPLICATION NUMBER: US 60/252767
PRIOR FILING DATE: 2000-11-22
NUMBER OF SEQ ID NOS: 574
SOFTWARE: PatentIn version 3.1
SEQ ID NO 250
LENGTH: 10

```

; TYPE: PRT
; ORGANISM: respiratory syncytial virus
US-10-432-234A-250
Query Match          39.5%; Score 32; DB 4; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 NDSPIDQTTDQ 10
        |||||
        1 NDMPITNDQ 9

Db

RESULT 8
US-10-155-693-29
; Sequence 29, Application US/10155693
; Publication No. US20030175876A1
; GENERAL INFORMATION:
; APPLICANT: FOX, GARY M.
; APPLICANT: JING, SHUOJIAN
; TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
; FILE REFERENCE: A-401C
; CURRENT APPLICATION NUMBER: US/10/155,693
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US/08/837,199
; PRIOR FILING DATE: 1997-04-14
; PRIOR APPLICATION NUMBER: US 60/015,907
; PRIOR FILING DATE: 1996-04-22
; PRIOR APPLICATION NUMBER: US 60/017,221
; PRIOR FILING DATE: 1996-05-09
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 14
; TYPE: PRT
; ORGANISM: RAT
US-10-155-693-29

Query Match          38.3%; Score 31; DB 4; Length 14;
Best Local Similarity 60.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      5 PIOTDQYTTT 14
        |||||
        4 PVQTTTATTT 13

Db

RESULT 9
US-10-872-161-29
; Sequence 29, Application US/10872161
; Publication No. US20040235714A1
; GENERAL INFORMATION:
; APPLICANT: FOX, GARY M.
; APPLICANT: JING, SHUOJIAN
; APPLICANT: WEN, DUANZHI
; TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
; FILE REFERENCE: A-401D
; CURRENT APPLICATION NUMBER: US/10/872,161
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: US/08/866,354
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: US 60/015,907
; PRIOR FILING DATE: 1996-04-22
; PRIOR APPLICATION NUMBER: US 60/017,221
; PRIOR FILING DATE: 1996-05-09
; PRIOR APPLICATION NUMBER: US 08/837,199
; PRIOR FILING DATE: 1997-04-14
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 14
; TYPE: PRT
```

```

; ORGANISM: RAT
US-10-872-161-29
Query Match          38.3%; Score 31; DB 5; Length 14;
Best Local Similarity 60.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      5 PIOTDQYTTT 14
        |||||
        4 PVQTTTATTT 13

Db

RESULT 10
US-10-462-452-433
; Sequence 433, Application US/10462452
; Publication No. US20040037809A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven
; APPLICANT: El Shafy, Mohammed Abd
; APPLICANT: Gupta, Malini
; APPLICANT: de Weireles, Jorge
; TITLE OF INVENTION: Compositions and Methods for Enhanced
; FILE REFERENCE: 02-02US
; CURRENT APPLICATION NUMBER: US/10/462,452
; PRIOR FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/393,066
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 790
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 433
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-462-452-433

Query Match          35.8%; Score 29; DB 4; Length 10;
Best Local Similarity 62.5%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 NDSPIDQTT 9
        |||||
        1 NDVPLPTD 8

Db

RESULT 11
US-10-601-953-561
; Sequence 561, Application US/10601953
; Publication No. US20040077540A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven C.
; TITLE OF INVENTION: Compositions And Methods For Modulating Physiology Of Epithelial
; TITLE OF INVENTION: Junctional Adhesion Molecules For Enhanced Mucosal Delivery Of
; FILE REFERENCE: 02-03US
; CURRENT APPLICATION NUMBER: US/10/601,953
; PRIOR FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: 60/392,512
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 900
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 561
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-601-953-561

Query Match          35.8%; Score 29; DB 4; Length 10;
Best Local Similarity 62.5%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

QY 2 NDSP1QTD 9
|||:|
Db 1 NDVPLPTD 8

RESULT 12
US-10-322-266-434
; Sequence 434, Application US/10322266
; Publication No. US20040115135A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven C.
; TITLE OF INVENTION: Compositions And Methods For Enhanced Mucosal Delivery Of Peptide
; FILE REFERENCE: NPE10567
; CURRENT APPLICATION NUMBER: US/10/322,266
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 797
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 434
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-322-266-434

Query Match 35.8%; Score 29; DB 4; Length 10;
Best Local Similarity 62.5%; Pred. No. 3.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSP1QTD 9
|||:|
Db 1 NDVPLPTD 8

RESULT 13
US-09-990-832C-108
; Sequence 108, Application US/09990832C
; Publication No. US20030149235A1
; GENERAL INFORMATION:
; APPLICANT: University Court of the University of Glasgow
; TITLE OF INVENTION: Targeting peptides
; FILE REFERENCE: PC/MC/JM/P11910US
; CURRENT APPLICATION NUMBER: US/09/990,832C
; CURRENT FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 108
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Targeting peptide sequence
US-09-990-832C-108

Query Match 35.8%; Score 29; DB 3; Length 12;
Best Local Similarity 62.5%; Pred. No. 4.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 SPIQTDQY 11
:|:|:|
Db 2 TP1QSTQY 9

RESULT 14
US-10-758-165-4
; Sequence 4, Application US/10758165
; Publication No. US20050196816A1
; GENERAL INFORMATION:
; APPLICANT: Hammerberg, Bruce
; TITLE OF INVENTION: IMMUNOGLOBULIN E DETECTION IN MAMMALIAN SPECIES
; FILE REFERENCE: 5051-661
; CURRENT APPLICATION NUMBER: US/10/758,165

; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: US 60/440,472
; PRIOR FILING DATE: 2003-01-16
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Ovis aries
US-10-758-165-4

Query Match 35.8%; Score 29; DB 5; Length 15;
Best Local Similarity 42.9%; Pred. No. 5.6e+02;
Matches 6; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 RNDSP1QTDQYTTT 14
|||:|:|
Db 1 RNKELMRGQHTTT 14

RESULT 15
US-10-462-452-457
; Sequence 457, Application US/10462452
; Publication No. US20040037809A1
; GENERAL INFORMATION:
; APPLICANT: Quay, Steven
; APPLICANT: Gupta, Mohammed Abd
; APPLICANT: de Meireles, Jorge
; TITLE OF INVENTION: Compositions and Methods for Enhanced
; FILE REFERENCE: 02-02US
; CURRENT APPLICATION NUMBER: US/10/462,452
; CURRENT FILING DATE: 2003-06-16
; PRIOR APPLICATION NUMBER: 60/393,066
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 790
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 457
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-462-452-457

Query Match 34.6%; Score 28; DB 4; Length 8;
Best Local Similarity 62.5%; Pred. No. 1.9e+06;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 RNDSP1QTD 8
|||:|
Db 1 RNDVPLPT 8

Search completed: May 30, 2006, 10:24:42
Job time : 48 secs

GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 30, 2006, 10:22:25 ; Search time 5.66667 Seconds
(without alignments)
29.481 Million cell updates/sec

Title: US-10-758-165A-1
Sequence: 1 RNDSPITQDTYTTG 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 56051 seqs, 11137335 residues

Total number of hits satisfying chosen parameters: 10973

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA New:*

- 1: /EMC_Celerra_SIDS3/ptocdata/1/pubppaa/US09_NEW_PUB pep:*
- 2: /EMC_Celerra_SIDS3/ptocdata/1/pubppaa/US06_NEW_PUB pep:*
- 3: /EMC_Celerra_SIDS3/ptocdata/1/pubppaa/US07_NEW_PUB pep:*
- 4: /EMC_Celerra_SIDS3/ptocdata/1/pubppaa/US08_NEW_PUB pep:*
- 5: /EMC_Celerra_SIDS3/ptocdata/1/pubppaa/US09_NEW_PUB pep:*
- 6: /EMC_Celerra_SIDS3/ptocdata/1/pubppaa/US10_NEW_PUB pep:*
- 7: /EMC_Celerra_SIDS3/ptocdata/1/pubppaa/US11_NEW_PUB pep:*
- 8: /EMC_Celerra_SIDS3/ptocdata/1/pubppaa/US60_NEW_PUB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	24	29.6	10	6	US-10-538-066-163
2	23	28.4	7	6	US-10-522-043-2
3	23	28.4	9	7	US-11-140-487A-1766
4	22	27.2	7	6	US-10-525-817-129
5	22	27.2	10	6	US-10-516-079-74
6	22	27.2	11	6	US-10-540-431-11
7	22	27.2	13	6	US-11-121-282-157
8	22	27.2	15	7	US-11-140-487A-2207
9	22	27.2	15	7	US-11-140-487A-2231
10	21	25.9	9	7	US-11-140-487A-1810
11	21	25.9	10	7	US-11-219-563-93
12	21	25.9	15	6	US-10-490-949-19
13	21	25.9	15	7	US-11-140-487A-2219
14	20	24.7	7	6	US-10-489-071-6
15	20	24.7	7	6	US-10-525-817-130
16	20	24.7	11	6	US-10-507-060A-2
17	20	24.7	12	7	US-11-054-072-335
18	20	24.7	12	7	US-11-054-072-335
19	20	24.7	12	7	US-11-122-986-570
20	20	24.7	14	7	US-11-176-182-52
21	20	24.7	15	7	US-11-176-182-31
22	19	23.5	7	7	US-11-023-959A-11
23	19	23.5	7	7	US-11-023-959A-14
24	19	23.5	9	6	US-10-538-066-174
25	19	23.5	10	6	US-10-516-079-64

26	19	23.5	10	6	US-10-538-066-172	Sequence 172, App
27	19	23.5	11	6	US-10-540-431-6	Sequence 6, Appli
28	19	23.5	12	1	US-09-784-950-10	Sequence 10, Appli
29	19	23.5	12	7	US-11-176-182-112	Sequence 112, App
30	19	23.5	12	7	US-11-054-072-7056	Sequence 7056, Ap
31	19	23.5	12	7	US-11-054-072-7057	Sequence 7057, Ap
32	19	23.5	12	7	US-11-054-072-7058	Sequence 7058, Ap
33	19	23.5	12	7	US-11-054-072-7059	Sequence 7059, Ap
34	19	23.5	12	7	US-11-054-072-7060	Sequence 7060, Ap
35	19	23.5	12	7	US-11-054-072-7061	Sequence 7061, Ap
36	19	23.5	12	7	US-11-054-072-7062	Sequence 7062, Ap
37	19	23.5	12	7	US-11-054-072-7063	Sequence 7063, Ap
38	19	23.5	12	7	US-11-054-072-7064	Sequence 7064, Ap
39	19	23.5	12	7	US-11-054-072-7065	Sequence 7065, Ap
40	19	23.5	12	7	US-11-054-072-7066	Sequence 7066, Ap
41	19	23.5	12	7	US-11-054-072-7067	Sequence 7067, Ap
42	19	23.5	13	7	US-11-176-182-17	Sequence 17, Appli
43	19	23.5	13	7	US-11-054-072-5136	Sequence 5136, Ap
44	19	23.5	13	7	US-11-054-072-5137	Sequence 5137, Ap
45	19	23.5	13	7	US-11-054-072-5138	Sequence 5138, Ap

ALIGNMENTS

RESULT 1
US-10-538-066-163
; Sequence 163, Application US/10538066
; Publication No. US20060094649A1
; GENERAL INFORMATION:
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7, and -B44 Tumor Associated Antigen
; FILE REFERENCE: 2060.015PC06
; CURRENT APPLICATION NUMBER: US/10/538, 066
; CURRENT FILING DATE: 2005-06-09
; PRIOR APPLICATION NUMBER: US 60/432, 017
; PRIOR FILING DATE: 2002-12-10
; NUMBER OF SEQ ID NOS: 767
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 163
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-538-066-163

Query Match 29.6%; Score 24; DB 6; Length 10;
Best Local Similarity 66.7%; Pred. No. 65;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 DSPITQ 8
|||:
Db 3 DSPITQ 8

RESULT 2
US-10-522-043-2
; Sequence 2, Application US/10522043
; Publication No. US20060100143A1
; GENERAL INFORMATION:
; APPLICANT: Lu et al.
; TITLE OF INVENTION: Polypeptide
; FILE REFERENCE: 69856
; CURRENT APPLICATION NUMBER: US/10/522, 043
; CURRENT FILING DATE: 2005-01-19
; PRIOR APPLICATION NUMBER: PCT/GB03/04296
; PRIOR FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 0306261.9
; PRIOR FILING DATE: 2003-03-19
; PRIOR APPLICATION NUMBER: 0223193.4
; PRIOR FILING DATE: 2002-10-07
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p53 inhibitor peptide
US-10-522-043-2

Query Match          28.4%; Score 23; DB 6; Length 7;
Best Local Similarity 57.1%; Pred. No. 5.2e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY      3 DSPIQTD 9      ||||
Db      1 DGPETD 7

RESULT 3
US-11-140-487A-1766
; Sequence 1766, Application US/11140487A
; Publication No. US20060093617A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C vi
; FILE REFERENCE: 166
; CURRENT APPLICATION NUMBER: US/11/140,487A
; PRIOR FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: EP 04012951.2
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: EP 04447239.7
; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: EP 05102441.2
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/576,310
; PRIOR FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: US 60/622,782
; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US 60/665,395
; NUMBER OF SEQ ID NOS: 2278
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 1766
; LENGTH: 9
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-11-140-487A-1766

Query Match          28.4%; Score 23; DB 7; Length 9;
Best Local Similarity 57.1%; Pred. No. 5.2e+04;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY      4 SPIOTDQ 10    ||||
Db      1 SPLTTNQ 7

RESULT 4
US-10-525-817-129
; Sequence 129, Application US/10525817
; Publication No. US20060099592A1
; GENERAL INFORMATION:
; APPLICANT: Nuevolution A/S
; TITLE OF INVENTION: Enzymatic encoding
; FILE REFERENCE: P912PC00
; CURRENT APPLICATION NUMBER: US/10/525,817
; CURRENT FILING DATE: 2005-02-25
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 129
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: Artificially produced
US-10-525-817-129

Query Match          27.2%; Score 22; DB 6; Length 7;
Best Local Similarity 80.0%; Pred. No. 5.2e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      1 RNDSP 5       ||||
Db      2 RGDSP 6

RESULT 5
US-10-516-079-74
; Sequence 74, Application US/10516079
; Publication No. US20060088899A1
; GENERAL INFORMATION:
; APPLICANT: ALVAREZ, Vernon L.
; APPLICANT: GRIMES, Carol A.
; APPLICANT: GORDA, Matthew A.
; TITLE OF INVENTION: Combination chemotherapy with chlorotoxin
; FILE REFERENCE: 51530-5006-MO
; CURRENT APPLICATION NUMBER: US/10/516,079
; CURRENT FILING DATE: 2004-11-29
; PRIOR APPLICATION NUMBER: US 60/406,033
; PRIOR FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: US 60/384,171
; PRIOR FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 74
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Pep21-SCXP_ANDMA sequence
US-10-516-079-74

Query Match          27.2%; Score 22; DB 6; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY      8 TDQYT 12      ||||
Db      2 TDQYT 6

RESULT 6
US-10-540-431-11
; Sequence 11, Application US/10540431
; Publication No. US20060089307A1
; GENERAL INFORMATION:
; APPLICANT: Amersham Health AS
; TITLE OF INVENTION: Contrast Agents
; FILE REFERENCE: PNO273
; CURRENT APPLICATION NUMBER: US/10/540,431
; CURRENT FILING DATE: 2005-06-22
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 11
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-540-431-11

Query Match          27.2%; Score 22; DB 6; Length 11;
Best Local Similarity 66.7%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY      10 QYTTG 15     |||||
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Db 2 QYADG 7

RESULT 7
US-11-121-282-197
; Sequence 197, Application US/11121282
; Publication No. US20060094862A1
; GENERAL INFORMATION:
; APPLICANT: Matti Salberg
; APPLICANT: Jan-Ingemar Floock
; TITLE OF INVENTION: SPECIFICITY EXCHANGERS THAT REDIRECT
; TITLE OF INVENTION: ANTIBODIES TO A PATHOGEN
; FILE REFERENCE: TRIPEP.7AUC4CPIC
; CURRENT APPLICATION NUMBER: US/11/121,282
; CURRENT FILING DATE: 2005-05-03
; PRIOR APPLICATION NUMBER: 10/372,735
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: 10/234,579
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: 09/839,666
; PRIOR FILING DATE: 2001-04-19
; PRIOR APPLICATION NUMBER: 09/532,106
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 09/664,945
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/246,258
; PRIOR FILING DATE: 1999-02-08
; NUMBER OF SEQ ID NOS: 199
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 197
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially Synthesized Peptides
US-11-121-282-197

Query Match 27.2%; Score 22; DB 7; Length 13;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 RNDSP 5
| | | |
Db 2 RGDSP 6

RESULT 8
US-11-140-487A-2207
; Sequence 2207, Application US/11140487A
; Publication No. US20060093617A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C vi
; FILE REFERENCE: 166
; CURRENT APPLICATION NUMBER: US/11/140,487A
; CURRENT FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: EP 04012951.2
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: EP 04447239.7
; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: EP 05102441.2
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/576,310
; PRIOR FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: US 60/622,782
; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US 60/665,395
; PRIOR FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2278
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2207
; LENGTH: 15
; TYPE: PRT

; ORGANISM: hepatitis C virus
US-11-140-487A-2207

Query Match 27.2%; Score 22; DB 7; Length 15;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 SPIQTD 9
| | | |
Db 2 SPVFTD 7

RESULT 9
US-11-140-487A-2231
; Sequence 2231, Application US/11140487A
; Publication No. US20060093617A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C vi
; FILE REFERENCE: 166
; CURRENT APPLICATION NUMBER: US/11/140,487A
; CURRENT FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: EP 04012951.2
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: EP 04447239.7
; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: EP 05102441.2
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/576,310
; PRIOR FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: US 60/622,782
; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US 60/665,395
; PRIOR FILING DATE: 2005-03-25
; NUMBER OF SEQ ID NOS: 2278
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2231
; LENGTH: 15
; TYPE: PRT
; ORGANISM: hepatitis C virus
US-11-140-487A-2231

Query Match 27.2%; Score 22; DB 7; Length 15;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 SPIQTD 9
| | | |
Db 10 SPVFTD 15

RESULT 10
US-11-140-487A-1810
; Sequence 1810, Application US/11140487A
; Publication No. US20060093617A1
; GENERAL INFORMATION:
; APPLICANT: Innogenetics N.V.
; TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C vi
; FILE REFERENCE: 166
; CURRENT APPLICATION NUMBER: US/11/140,487A
; CURRENT FILING DATE: 2005-05-31
; PRIOR APPLICATION NUMBER: EP 04012951.2
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: EP 04447239.7
; PRIOR FILING DATE: 2004-10-28
; PRIOR APPLICATION NUMBER: EP 05102441.2
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: US 60/576,310
; PRIOR FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: US 60/622,782
; PRIOR FILING DATE: 2004-10-29
; PRIOR APPLICATION NUMBER: US 60/665,395
; PRIOR FILING DATE: 2005-03-25

NUMBER OF SEQ ID NOS: 2278
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1810
LENGTH: 9
TYPE: PRT
ORGANISM: hepatitis C virus
US-11-140-487A-1810

Query Match 25.9%; Score 21; DB 7; Length 9;
Best Local Similarity 80.0%; Pred. No. 5.2e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 YTTTG 15
|||
Db 2 YTTTG 6

RESULT 11
US-11-219-563-93
Sequence 93, Application US/11219563
Publication No. US20060088539A1
GENERAL INFORMATION:
APPLICANT: Bander, Neil
TITLE OF INVENTION: MODIFIED ANTIBODIES TO PROSTATE-SPECIFIC
FILE REFERENCE: 13651.001 (B2L-001)
CURRENT APPLICATION NUMBER: US/11/219,563
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: PCT/US04/06586
PRIOR FILING DATE: 2004-03-03
PRIOR APPLICATION NUMBER: US 10/379,838
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: 10/449,379
PRIOR FILING DATE: 2003-05-30
NUMBER OF SEQ ID NOS: 144
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 93
LENGTH: 10
TYPE: PRT
ORGANISM: Mus musculus
US-11-219-563-93

Query Match 25.9%; Score 21; DB 7; Length 10;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 YTTTG 15
|||
Db 2 YTTTG 6

RESULT 12
US-10-490-949-19
Sequence 19, Application US/10490949
Publication No. US20060093574A1
GENERAL INFORMATION:
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: ALBANI, Salvatore
APPLICANT: MARTINI, Alberto
TITLE OF INVENTION: METHODS FOR EPITOPE-SPECIFIC AND CYTOKINE/ANTICYTOKINE
TITLE OF INVENTION: COMBINATION IMMUNOTHERAPIES FOR MODULATION OF PATHOGENIC
FILE REFERENCE: US041450-2
CURRENT APPLICATION NUMBER: US/10/490,949
CURRENT FILING DATE: 2004-03-25
PRIOR APPLICATION NUMBER: PCT/US02/30578
PRIOR FILING DATE: 2002-09-25
PRIOR APPLICATION NUMBER: US 60/339,284
PRIOR FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: US 60/325,499
PRIOR FILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn version 3.1

SEQ ID NO 19
LENGTH: 15
TYPE: PRT
ORGANISM: Homo sapiens
US-10-490-949-19

Query Match 25.9%; Score 21; DB 6; Length 15;
Best Local Similarity 57.1%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 DQYTTTG 15
|||
Db 2 DQYTTTG 8

RESULT 13
US-11-140-487A-2219
Sequence 2219, Application US/11140487A
Publication No. US20060093617A1
GENERAL INFORMATION:
APPLICANT: Innogenetics N.V.
TITLE OF INVENTION: Peptides for inducing a CTL and/or HTL response to Hepatitis C vi
FILE REFERENCE: 166
CURRENT APPLICATION NUMBER: US/11/140,487A
CURRENT FILING DATE: 2005-05-31
PRIOR APPLICATION NUMBER: EP 04012951.2
PRIOR FILING DATE: 2004-06-01
PRIOR APPLICATION NUMBER: EP 04447239.7
PRIOR FILING DATE: 2004-10-28
PRIOR APPLICATION NUMBER: EP 05102441.2
PRIOR FILING DATE: 2005-03-25
PRIOR APPLICATION NUMBER: US 60/576,310
PRIOR FILING DATE: 2004-06-03
PRIOR APPLICATION NUMBER: US 60/622,782
PRIOR FILING DATE: 2004-10-29
PRIOR APPLICATION NUMBER: US 60/665,395
PRIOR FILING DATE: 2005-03-25
NUMBER OF SEQ ID NOS: 2278
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2219
LENGTH: 15
TYPE: PRT
ORGANISM: hepatitis C virus
US-11-140-487A-2219

Query Match 25.9%; Score 21; DB 7; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.5e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 YTTTG 15
|||
Db 2 YTTTG 6

RESULT 14
US-10-489-071-6
Sequence 6, Application US/10489071
Publication No. US20060094672A1
GENERAL INFORMATION:
APPLICANT: PASQUALINE ET AL.
TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE OF TARGETING PEPTIDES AGAINST
TITLE OF INVENTION: PLACENTA AND ADIPOSE TISSUES
FILE REFERENCE: UTSC:856US
CURRENT APPLICATION NUMBER: US/10/489,071
CURRENT FILING DATE: 2004-03-08
PRIOR APPLICATION NUMBER: PCT/US02/27836
PRIOR FILING DATE: 2002-08-30
NUMBER OF SEQ ID NOS: 144
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-489-071-6

Query Match 24.7%; Score 20; DB 6; Length 7;
Best Local Similarity 42.9%; Pred. No. 5.2e+04;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RNDSPQ 7
| | | | |
| | | | |
Db 1 RMDGPVR 7

RESULT 15
US-10-525-817-130
; Sequence 130; Application US/10525817
; Publication No. US20060093592A1
; GENERAL INFORMATION:
; APPLICANT: Nuevolution A/S
; TITLE OF INVENTION: Enzymatic encoding
; FILE REFERENCE: P912PC00
; CURRENT APPLICATION NUMBER: US/10/525,817
; CURRENT FILING DATE: 2005-02-25
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 130
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially produced
US-10-525-817-130

Query Match 24.7%; Score 20; DB 6; Length 7;
Best Local Similarity 80.0%; Pred. No. 5.2e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RNDSP 5
| | | | |
| | | | |
Db 2 RADSP 6

Search completed: May 30, 2006, 10:25:04
Job time : 5.66667 secs

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GenCore version 5.1.8
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OM protein - protein search, using sw model

Run on: May 30, 2006, 09:59:16 ; Search time 20.3333 Seconds

(without alignments)
64.572 Million cell updates/sec

Title: US-10-758-165A-1

Perfect score: 81
Sequence: 1 RNDSPIDQDTTGG 15Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 249102

Minimum DB seq length: 0
Maximum DB seq length: 15Post-processing: Minimum Match 0%
Maximum Match 100%

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3: /EMC_Celerra_SIDS3/prodata/2/iaa/7 COMB.pep.*
4: /EMC_Celerra_SIDS3/prodata/2/iaa/H COMB.pep.*
5: /EMC_Celerra_SIDS3/prodata/2/iaa/PCUS COMB.pep.*
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7: /EMC_Celerra_SIDS3/prodata/2/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	39.5	13	7 5223254-6	Patent No. 5223254
2	31	38.3	14	2 US-08-837-199A-29	Sequence 29, Appl
3	28.5	35.2	15	3 US-09-641-528B-48206	Sequence 48206, A
4	28	34.6	9	3 US-09-641-528B-5634	Sequence 5634, Ap
5	28	34.6	9	3 US-09-641-528B-10412	Sequence 10412, A
6	28	34.6	9	3 US-09-641-528B-35442	Sequence 35442, A
7	28	34.6	9	3 US-09-641-528B-42435	Sequence 42435, A
8	28	34.6	9	3 US-09-641-528B-51014	Sequence 51014, A
9	28	34.6	10	3 US-09-641-528B-5507	Sequence 5507, Ap
10	28	34.6	10	3 US-09-641-528B-10417	Sequence 10417, A
11	28	34.6	10	3 US-09-641-528B-35452	Sequence 35452, A
12	28	34.6	10	3 US-09-641-528B-12443	Sequence 12443, A
13	28	34.6	11	3 US-09-641-528B-5635	Sequence 5635, Ap
14	28	34.6	11	3 US-09-641-528B-10352	Sequence 10352, A
15	28	34.6	11	3 US-09-641-528B-35263	Sequence 35263, A
16	28	34.6	11	3 US-09-641-528B-42319	Sequence 42319, A
17	28	34.6	11	3 US-09-641-528B-42319	Sequence 42319, A
18	28	34.6	15	3 US-09-641-528B-47375	Sequence 47375, A
19	28	34.6	15	3 US-09-641-528B-50683	Sequence 50683, A
20	27	33.3	9	2 US-09-341-982-75	Sequence 75, Appl
21	27	33.3	12	1 US-08-479-233-8	Sequence 8, Appl
22	27	33.3	12	1 PCT-US93-00643-8	Sequence 8, Appl
23	27	33.3	13	1 US-08-209-525-50	Sequence 50, Appl
24	26	32.1	15	2 US-09-914-259-161	Sequence 161, App
25	26	32.1	9	3 US-09-641-528B-4318	Sequence 4318, App
26	26	32.1	9	3 US-09-641-528B-50956	Sequence 50956, A
27	26	32.1	10	3 US-09-641-528B-4238	Sequence 4238, Ap

ALIGNMENTS

27	26	32.1	11	3	US-09-641-528B-4319	Sequence 4319, Ap
28	26	32.1	12	1	US-08-423-441-4	Sequence 4, Appl
29	26	32.1	12	2	US-09-514-739-5	Sequence 5, Appl
30	26	32.1	12	2	US-09-517-866-13	Sequence 13, Appl
31	26	32.1	12	2	US-10-279-991A-13	Sequence 1, Appl
32	26	32.1	15	2	US-10-378-707-1	Sequence 50625, A
33	26	32.1	15	3	US-09-641-528B-50625	Sequence 4, Appl
34	25	30.9	8	3	US-08-413-708B-4	Sequence 10393, A
35	25	30.9	8	3	US-09-641-528B-10393	Sequence 35388, A
36	25	30.9	8	3	US-09-641-528B-35388	Sequence 42396, A
37	25	30.9	9	3	US-09-641-528B-42396	Sequence 5590, Ap
38	25	30.9	11	1	US-09-641-528B-5590	Sequence 2, Appl
39	25	30.9	11	1	US-08-077-939-2	Sequence 2, Appl
40	25	30.9	11	1	US-08-461-599-2	Sequence 24, Appl
41	25	30.9	11	1	US-07-949-812-24	Sequence 2, Appl
42	25	30.9	11	1	US-08-461-621-2	Sequence 2, Appl
43	25	30.9	11	1	US-08-465-334-2	Sequence 5591, Ap
44	25	30.9	11	3	US-09-641-528B-5591	Sequence 14203, A
45	25	30.9	11	3	US-09-641-528B-14203	

RESULT 1
5223254-6
Patent No. 5223254
APPLICANT: PARADISO, PETER R.; HILDRETH, STEPHEN W.; HU, BRADA T.; MARTIN-GALLARDO, ANTONIA; ARUMUGHAN, RASAPPA
TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS VACCINES
NUMBER OF SEQUENCES: 17
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/247,017
FILING DATE: 20-SEP-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 102,180
FILING DATE: 29-SEP-1987
SEQ ID NO: 6;
LENGTH: 13
5223254-6

Query Match 39.5%; Score 32; DB 7; Length 13;
Best Local Similarity 66.7%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 NDSPIDQ 10
DB 2 NDMPITNDQ 10

RESULT 2
US-08-837-199A-29
Sequence 29, Application US/08837199A
Patent No. 6455277
GENERAL INFORMATION:
APPLICANT: FOX, GARY M.
APPLICANT: JING, SHUOJIAN
APPLICANT: WEN, DUANZHI
TITLE OF INVENTION: GLIAL CELL LINE-DERIVED NEUROTROPHIC FACTOR RECEPTOR
FILE REFERENCE: A-401C
CURRENT APPLICATION NUMBER: US/08/837,199A
CURRENT FILING DATE: 1997-04-14
PRIOR APPLICATION NUMBER: US 60/015,907
PRIOR FILING DATE: 1996-04-22
PRIOR APPLICATION NUMBER: US 60/017,221
PRIOR FILING DATE: 1996-05-09
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn version 3.1
SEQ ID NO 29
LENGTH: 14
TYPE: PRT
ORGANISM: RAT
US-08-837-199A-29

Query Match 38.3%; Score 31; DB 2; Length 14;
Best Local Similarity 60.0%; Pred. No. 58;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 5 IQTDOYTT 14
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Db 4 PVQTTATTT 13

RESULT 3
US-09-641-528B-48206
; Sequence 48206, Application US/09641528B
; Patent No. 7026443

; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48206
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus

US-09-641-528B-48206

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Matches 6; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

OY 2 NDSPQOT-DOYTT 13
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Db 3 NVSEVETVNEYNT 15

RESULT 4
US-09-641-528B-5634
; Sequence 5634, Application US/09641528B
; Patent No. 7026443

; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5634
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus

US-09-641-528B-5634

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Best Local Similarity 50.0%; Pred. No. 5e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 6 IQTDOYTT 13
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Db 2 VSTDEYVT 9

RESULT 5
US-09-641-528B-10412
; Sequence 10412, Application US/09641528B
; Patent No. 7026443

; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10412
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus

US-09-641-528B-10412

Query Match 34.6%; Score 28; DB 3; Length 9;
Best Local Similarity 50.0%; Pred. No. 5e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 6 IQTDOYTT 13
: ||| |
Db 1 VSTDEYVT 8

RESULT 6
US-09-641-528B-35442
; Sequence 35442, Application US/09641528B
; Patent No. 7026443

; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35442
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus

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; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
; US-09-641-528B-35442
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Best Local Similarity 50.0%; Pred. No. 5e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      6 IQTDOYTT 13
       : ||: ||
Db      1 VSTDENVY 8

RESULT 7
US-09-641-528B-42435
; Sequence 42435, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641.528B
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42435
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
; US-09-641-528B-42435
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Best Local Similarity 50.0%; Pred. No. 5e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      6 IQTDOYTT 13
       : ||: ||
Db      1 VSTDENVY 8

RESULT 8
US-09-641-528B-51014
; Sequence 51014, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641.528B
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51014
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
; US-09-641-528B-51014
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Best Local Similarity 50.0%; Pred. No. 5e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      6 IQTDOYTT 13
       : ||: ||
Db      1 VSTDENVY 8

RESULT 9
US-09-641-528B-5507
; Sequence 5507, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641.528B
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5507
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
; US-09-641-528B-5507
Query Match          34.6%; Score 28; DB 3; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      6 IQTDOYTT 13
       : ||: ||
Db      3 VSTDENVY 10

RESULT 10
US-09-641-528B-10417
; Sequence 10417, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641.528B
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10417
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-10417

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Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 IQTDOYTT 13
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Db 2 VSTDENVYV 9

RESULT 11
US-09-641-528B-35452
; Sequence 35452, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641.528B
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35452
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-35452

Query Match          34.6%; Score 28; DB 3; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 IQTDOYTT 13
   : ||: ||
Db 2 VSTDENVYV 9

RESULT 12
US-09-641-528B-42443
; Sequence 42443, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641.528B
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42443
; LENGTH: 10
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-42443

Query Match          34.6%; Score 28; DB 3; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 IQTDOYTT 13
   : ||: ||
Db 2 VSTDENVYV 9

RESULT 13
US-09-641-528B-5635
; Sequence 5635, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641.528B
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5635
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-5635

Query Match          34.6%; Score 28; DB 3; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 IQTDOYTT 13
   : ||: ||
Db 2 VSTDENVYV 9

RESULT 14
US-09-641-528B-10362
; Sequence 10362, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641.528B
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10362
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; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-10362

Query Match      34.6%; Score 28; DB 3; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      6 IQTDPYTT 13
      : ||: ||
Db      3 VSTDEYVT 10

RESULT 15
US-09-641-528B-35263
; Sequence 35263, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Eteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528B
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51505
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35263
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-35263

Query Match      34.6%; Score 28; DB 3; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Db      3 VSTDEYVT 10
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Title: US-10-758-165A-1
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Sequence: 1 RNDSP1QTDQYTTTG 15

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4: pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	34.6	14	2	PH1306
2	26	32.1	11	2	S71304
3	24	29.6	14	2	PS0249
4	22	27.2	14	2	PH1305
5	21	25.9	11	2	PS0259
6	21	25.3	13	2	H56046
7	20.5	25.3	13	2	S47376
8	20	24.7	11	2	S04875
9	20	24.7	11	2	A26120
10	20	24.7	11	2	S05002
11	20	24.7	12	2	PH0771
12	20	24.7	13	2	PM0125
13	20	24.7	10	1	PH1347
14	19	23.5	10	1	GMR012
15	19	23.5	10	2	B60656
16	19	23.5	11	2	SS8244
17	19	23.5	13	2	B61458
18	19	23.5	13	2	A61458
19	19	23.5	14	2	PH1705
20	19	23.5	14	2	SS0900
21	19	23.5	15	2	S42741
22	19	23.5	15	2	PH1631
23	18	22.2	7	2	I48086
24	18	22.2	10	2	S43625
25	18	22.2	12	2	A61332
26	18	22.2	12	2	ES8502
27	18	22.2	12	2	A61503
28	18	22.2	13	2	A33660
29	18	22.2	13	2	PT0331

30	18	22.2	14	2	PT0232	Ig heavy chain CRD
31	18	22.2	15	2	S32677	nitrogenase cofact
32	18	22.2	15	2	PA0097	search phosphotyria
33	18	22.2	15	2	S29485	GTP-binding protei
34	18	22.2	15	2	S72432	epoxypropan isomer
35	17	21.0	8	2	I57018	gene Cfr protein
36	17	21.0	9	2	PT0247	Ig heavy chain CRD
37	17	21.0	9	2	PL0139	carbon-monoxide de
38	17	21.0	10	2	B61512	variant surface gl
39	17	21.0	11	2	C53652	rhlR protein - pse
40	17	21.0	11	2	A29806	acidic proline-ric
41	17	21.0	11	2	S42449	anti protein - pha
42	17	21.0	12	2	S25485	transcription fact
43	17	21.0	12	2	PT0228	Ig heavy chain CDR
44	17	21.0	12	2	JU0356	cycloleornitrin -
45	17	21.0	12	2	PM0170	alcohol dehydrogen

ALIGNMENTS

RESULT 1
PH1306
Ig heavy chain DJ region (clone C96-100) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1306
R:Masserman, R.; Galli, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A:Reference number: PH1302; MUID:93094761; PMID:1460419
A:Cross-references: UNIPARC:UPI000017C253
A:Molecule type: DNA
A:Residues: 1-14 <MAS>
A:Cross-references: UNIPARC:UPI000017C253
C:Keywords: heterotetramer; immunoglobulin

Query Match 34.6%; Score 28; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 YTTTG 15
DB 6 YTTTG 10

RESULT 2
S71304
amine oxidase (copper-containing) (EC 1.4.3.6) II - Aspergillus niger (fragment)
C:Species: Aspergillus niger
C:Date: 12-Feb-1998 #sequence_revision 01-May-1998 #text_change 09-Jul-2004
C:Accession: S71304
R:Fireborn, I.; Tamaki, H.; Ishida, H.; Pec, P.; Luhova, L.; Tauno, H.; Halata, M.; Asano
Eur. J. Biochem. 237, 255-265, 1996
A:Title: Two distinct quinoprotein amine oxidases are induced by n-butylamine in the myc
A:Reference number: S71303; MUID:96203933; PMID:8620882
A:Accession: S71304
A:Molecule type: protein
A:Residues: 1-11 <PRE>
A:Cross-references: UNIPROT:O7M504; UNIPARC:UPI000017B3B7
C:Keywords: copper binding; monomer; oxidoreductase; quinoprotein; topaquione

Query Match 32.1%; Score 26; DB 2; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 NDSP1QTD 9
DB 1 NDSPALND 8

RESULT 3
PS0249

porin - rice (strain Nihonbare) (fragment)

C:Species: Oryza sativa (rice)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004

C:Accession: PS0249

R:Teugita, A.

submitted to JIPID, April 1993

A:Reference number: PS0206

A:Accession: PS0249

A:Molecule type: protein

A:Residues: 1-14 <TSU>

A:Cross-references: UNIPROT:Q7M1U8; UNIPARC:UPI000017B118

A:Experimental source: callus

Query Match 29.6%; Score 24; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 4.8e+02;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 8 TDQYTTG 15
| | | | |

Db 5 TDDHTANG 12
| | | | |

RESULT 4

PH1305

Ig heavy chain DJ region (clone C85-1B) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C:Accession: PH1305

R:Wasserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

J. Exp. Med. 176, 1577-1581, 1992

A:Title: Predominance of fetal type DJH joining in young children with B precursor lymph

A:Reference number: PH1302; MUID:93094761; PMID:1460419

A:Accession: PH1305

A:Molecule type: DNA

A:Residues: 1-14 <WAS>

A:Cross-references: UNIPARC:UPI000017C252

C:Keywords: heterotetramer; immunoglobulin

Query Match 27.2%; Score 22; DB 2; Length 14;
Best Local Similarity 62.5%; Pred. No. 1.1e+03;

Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 6 IQFDQYTT 13
| | | | |

Db 2 ILTGYYTT 9
| | | | |

RESULT 5

PS0259

39K protease 3225 - rice (strain Nihonbare) (fragment)

C:Species: Oryza sativa (rice)

C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 11-Apr-1995

C:Accession: PS0259

R:Teugita, A.; Kamo, M.

submitted to JIPID, April 1993

A:Reference number: PS0209

A:Accession: PS0259

A:Molecule type: protein

A:Residues: 1-11 <TSU>

A:Cross-references: UNIPARC:UPI000017B102

A:Experimental source: callus

C:Comment: molecular weight 39K, pI 5.7.

Query Match 25.9%; Score 21; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 1.3e+03;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 3 DSPIQTD 9
| | | | |

Db 5 DGPIVAD 11
| | | | |

RESULT 6

H56046

urinary tract stone matrix protein 10, 42k - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 09-Jul-2004

C:Accession: H56046

R:Binet, J.P.; Binette, M.B.; Gawinowicz, M.A.; Kendrick, N.

submitted to the Protein Sequence Database, February 1995

A:Description: Isolation, characterization and sequence of stone proteins.

A:Reference number: A56046

A:Accession: H56046

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-13 <BIN>

A:Cross-references: UNIPROT:Q7M4P7; UNIPARC:UPI000017C406

Query Match 25.9%; Score 21; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.5e+03;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 NDSPIQTD 9
| | | | |

Db 6 NDLAATD 13
| | | | |

RESULT 7

S47376

T-cell antigen receptor VJ junction beta chain - human

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999

C:Accession: S47376

R:Lehner, P.J.

submitted to the EMBL Data Library, August 1994

A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c

A:Reference number: S47355

A:Accession: S47376

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-13 <LEH>

A:Cross-references: UNIPARC:UPI0000116687; EMBL:Z35702; NID:G527497; PIDN:CAAB4771.1; PII

C:Keywords: T-cell receptor

Query Match 25.3%; Score 20.5; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.9e+03;

Matches 6; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY 4 SPIQTD-QY 11
| | | | |

Db 4 SPRSTDTQY 12
| | | | |

RESULT 8

S04875

nifs protein - Bradyrhizobium japonicum (fragment)

C:Species: Bradyrhizobium japonicum

C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004

C:Accession: S04875

R:Ebeling, S.

submitted to the EMBL Data Library, December 1988

A:Reference number: S04873

A:Accession: S04875

A:Molecule type: DNA

A:Residues: 1-11 <EBE>

A:Cross-references: UNIPROT:P37030; UNIPARC:UPI000016E719; EMBL:X13691; NID:G39544; PIDN

C:Genetics:

A:Gene: nifs

A:Start codon: GTG

Query Match 24.7%; Score 20; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.9e+03;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 NDSPIQTD 9
| | | | |

Db 4 NRAPTYLD 11

RESULT 9

A26120

6-phosphofructokinase (EC 2.7.1.11) - pig roundworm (fragment)
N:Alternate names: phosphofructokinase; phosphohexokinase

C:Species: Ascaris suum (pig roundworm)
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 09-Jul-2004

C:Accession: A26120

R:Kulkarni, G.; Rao, G.S.J.; Srinivasan, N.G.; Hofer, H.W.; Yuan, P.M.; Harris, B.G.

J. Biol. Chem. 262, 32-34, 1987

A:Title: Ascaris suum phosphofructokinase. Phosphorylation by protein kinase and sequenc

A:Reference number: A26120; MUID:87083467; PMID:3025208

A:Accession: A26120

A:Molecule type: protein

A:Residues: 1-11 <KUL>

A:Cross-references: UNIPROT:Q7M4J2; UNIPARC:UPI000017B699

C:Keywords: glycolysis; phosphotransferase

Query Match 24.7%; Score 20; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.9e+03;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 RNDSPICR 8

Db 4 RSDSIVPT 11

RESULT 10

S05002

corazonin - American cockroach

C:Species: Periplaneta americana (American cockroach)

C:Date: 07-Sep-1990 #sequence_revision 09-Apr-1998 #text_change 09-Jul-2004

C:Accession: S05002

R:Venestra, J.A.

FEBS Lett. 250, 231-234, 1989

A:Title: Isolation and structure of corazonin, a cardiodactive peptide from the american

A:Reference number: S05002; MUID:89325572; PMID:2753132

A:Accession: S05002

A:Molecule type: protein

A:Residues: 1-11 <VEE>

A:Cross-references: UNIPROT:P11496; UNIPARC:UPI0000127F28

C:Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:1/Modified site: amidated carboxyl end (Asn) #status experimental

Query Match 24.7%; Score 20; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 1.9e+03;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 7 QTDQYT 12

Db 1 QTFQYS 6

RESULT 11

PH0771

T-cell receptor beta chain (PE5.1.1) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999

C:Accession: PH0771

R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A:Title: T cell receptor genes in a series of class I major histocompatibility complex-
allelic exclusion and antigen-specific repertoire.

A:Reference number: PH0746; MUID:92078846; PMID:1836010

A:Accession: PH0771

A:Molecule type: mRNA

A:Residues: 1-12 <CNS>

A:Cross-references: UNIPARC:UPI0000115FBE; EMBL:X60865; NID:G53624; PIDN:CAA43255.1; PID

A:Experimental source: T lymphocyte

C:Keywords: T-cell receptor

Query Match 24.7%; Score 20; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.1e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 4 SPIQTDQY 11

Db 3 SSFQYEQY 10

RESULT 12

PN0125

serine proteinase (EC 3.4.21.-) - Actinomyces sp. (fragment)

C:Species: Actinomyces sp.

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C:Accession: PN0125

R:Mosolova, O.V.; Rudenskaya, G.N.; Stepanov, V.M.; Khodova, O.M.; Tsaplina, I.A.

Biohimia 52, 414-422, 1987

A:Title: Glu, Asp-specific proteinase from Actinomyces.

A:Reference number: PN0125

A:Accession: PN0125

A:Molecule type: protein

A:Residues: 1-13 <MOS>

A:Cross-references: UNIPROT:Q7M107; UNIPARC:UPI000017AD24

A:Note: article in Russian with English abstract

C:Keywords: hydrolase; serine proteinase

Query Match 24.7%; Score 20; DB 2; Length 13;
Best Local Similarity 62.5%; Pred. No. 2.3e+03;

Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 4 SPIQTDQY 11

Db 1 SVIGTDVY 8

RESULT 13

PH1347

Ig heavy chain DJ region (clone C100-103A) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C:Accession: PH1347

R:Wasserman, R.; Gallil, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

J. Exp. Med. 176, 1577-1581, 1992

A:Title: Predominance of fetal type DH joining in young children with B precursor lymph

A:Reference number: PH1302; MUID:93094761; PMID:1460419

A:Accession: PH1347

A:Molecule type: DNA

A:Residues: 1-14 <MAS>

A:Cross-references: UNIPARC:UPI000017C21C

C:Keywords: heterotrimer; immunoglobulin

Query Match 24.7%; Score 20; DB 2; Length 14;
Best Local Similarity 42.9%; Pred. No. 2.5e+03;

Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 9 DQYTTTG 15

Db 4 EDPLTTG 10

RESULT 14

GMR02

leucosulfakinin-II - Madeira cockroach

N:Alternate names: LSK-II

C:Species: Leucophaea maderae (Madeira cockroach)

C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004

C:Accession: A26335

R:Nachman, R.U.; Holman, G.M.; Cook, B.J.; Haddon, W.F.; Ling, N.

Biochem. Biophys. Res. Commun. 140, 357-364, 1986

A:Title: Leucosulfakinin-II, a blocked sulfated insect neuropeptide with homology to cho

A:Reference number: A26335; MUID:87048769; PMID:3778455

A:Accession: A26335

A;Molecule type: protein
A;Residues: 1-10 <NAC
A;Cross-references: UNIPROT:P09039, UNIPARC:UPI000012B961
C;Comment: This peptide was isolated from head extracts. It stimulates muscle contractile
C;Superfamily: gastrin
C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid; sulfoprotein
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;5/Binding site: sulfate (Tyr) (covalent) #status experimental
F;10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 23.5%; Score 19; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 QTDQY 11
|:|
1 QSDPY 5

RESULT 15

B60656
leucosulfakinin II, non-sulfated - American cockroach
C;Species: Periplaneta americana (American cockroach)
C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
C;Accession: B60656
R;Venestra, J.A.
Neuropeptides 14, 145-149, 1989
A;Title: Isolation and structure of two gastrin/CKK-like neuropeptides from the American
A;Reference number: A60656; MUID:90137190; PMID:2615921
A;Accession: B60656
A;Molecule type: protein
A;Residues: 1-10 <VEE>
A;Cross-references: UNIPROT:P09039, UNIPARC:UPI000012B961
C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 23.5%; Score 19; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 QTDQY 11
|:|
1 QSDPY 5

Search completed: May 30, 2006, 10:13:21
Job time : 12 secs


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RN NUCLEOTIDE SEQUENCE.
RC STRAIN=SP11, SP19, SP21, SP23, SP24, SP4, SP6, SP8, and SP9;
RX PubMed=1595661; DOI=10.1534/genetics.105.045120;
RA Borge T., Webster M.T., Anderson G., Saetre G.-P.;
RT "Contrasting Patterns of Polymorphism and Divergence on the Z
  Chromosome and Autosomes in Two Ficedula Flycatcher Species.";
RL Genetics 171:1861-1873(2005).
CC -----
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CC -----
DR EMBL; AJ869954; CA135707.1; -; Genomic DNA.
DR EMBL; AJ869955; CA135708.1; -; Genomic DNA.
DR EMBL; AJ869956; CA135709.1; -; Genomic DNA.
DR EMBL; AJ869957; CA135710.1; -; Genomic DNA.
DR EMBL; AJ869958; CA135711.1; -; Genomic DNA.
DR EMBL; AJ869959; CA135712.1; -; Genomic DNA.
DR EMBL; AJ869960; CA135713.1; -; Genomic DNA.
DR EMBL; AJ869961; CA135714.1; -; Genomic DNA.
DR EMBL; AJ869962; CA135715.1; -; Genomic DNA.
FT NON_TER
FT 1
SQ SEQUENCE 13 AA; 1635 MW; 7D3029BDE712DEA4 CRC64;

Query March 29.6%; Score 24; DB 2; Length 13;
Best Local Similarity 45.5%; Pred. No. 4.6e+03;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 3 DSP1QTDQYTT 13
Db 1 DHDLRQCQYVT 11

RESULT 3
Q2WDH5_FICAL PRELIMINARY; PRT; 13 AA.
ID Q2WDH5_FICAL
AC Q2WDH5;
DT 10-JUN-2006, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Aldolase B (Fragment).
GN Name=ab;
OS Ficedula albicollis (Collared flycatcher).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Muscicapidae; Ficedula.
OX NCBI_TaxID=59894;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=IC10, IC2, IC3, IC4, IC5, IC6, IC7, IC8, and IC9;
RX PubMed=1595661; DOI=10.1534/genetics.105.045120;
RA Borge T., Webster M.T., Anderson G., Saetre G.-P.;
RT "Contrasting Patterns of Polymorphism and Divergence on the Z
  Chromosome and Autosomes in Two Ficedula Flycatcher Species.";
RL Genetics 171:1861-1873(2005).
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DR EMBL; AJ869945; CA135698.1; -; Genomic DNA.
DR EMBL; AJ869946; CA135699.1; -; Genomic DNA.
DR EMBL; AJ869947; CA135700.1; -; Genomic DNA.
DR EMBL; AJ869948; CA135701.1; -; Genomic DNA.
DR EMBL; AJ869949; CA135702.1; -; Genomic DNA.
DR EMBL; AJ869950; CA135703.1; -; Genomic DNA.
DR EMBL; AJ869951; CA135704.1; -; Genomic DNA.
DR EMBL; AJ869952; CA135705.1; -; Genomic DNA.
DR EMBL; AJ869944; CA135697.1; -; Genomic DNA.
FT NON_TER
FT 1
SQ SEQUENCE 13 AA; 1635 MW; 7D3029BDE712DEA4 CRC64;

Query Match 29.6%; Score 24; DB 2; Length 13;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 3 DSP1QTDQYTT 13
Db 1 DHDLRQCQYVT 11
```

```

Best Local Similarity 45.5%; Pred. No. 4.6e+03;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 3 DSP1QTDQYTT 13
Db 1 DHDLRQCQYVT 11

RESULT 4
Q804K2_FICPA PRELIMINARY; PRT; 13 AA.
ID Q804K2_FICPA
AC Q804K2;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 8.
DE Aldolase B (Fragment).
GN Name=Aldob; Synonyms=ab;
OS Ficedula parva (Red-breasted flycatcher).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Muscicapidae; Ficedula.
OX NCBI_TaxID=126711;
RN NUCLEOTIDE SEQUENCE.
RP STRAIN=Parv;
RA Saetre G.-P., Borge T., Lindroos K., Haavie J., Sheldon B.C.,
RA Primer C.R., Svanen A.-C.;
RT "Sex chromosome evolution and speciation in Ficedula flycatchers.";
RL Proc. R. Soc. Lond., B, Biol. Sci. 0:0-0(2003).
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=Parv;
RX PubMed=1595661; DOI=10.1534/genetics.105.045120;
RA Borge T., Webster M.T., Anderson G., Saetre G.-P.;
RT "Contrasting Patterns of Polymorphism and Divergence on the Z
  Chromosome and Autosomes in Two Ficedula Flycatcher Species.";
RL Genetics 171:1861-1873(2005).
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CC -----
DR EMBL; AY154343; AA017275.1; -; Genomic DNA.
DR EMBL; AJ869953; CA135706.1; -; Genomic DNA.
FT NON_TER
FT 1
SQ SEQUENCE 13 AA; 1635 MW; 7D3029BDE712DEA4 CRC64;

Query March 29.6%; Score 24; DB 2; Length 13;
Best Local Similarity 45.5%; Pred. No. 4.6e+03;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 3 DSP1QTDQYTT 13
Db 1 DHDLRQCQYVT 11

RESULT 5
Q7M1U8_ORYSA PRELIMINARY; PRT; 14 AA.
ID Q7M1U8_ORYSA
AC Q7M1U8;
DT 15-DEC-2003, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 1.
DE Porin (Fragment).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
OC Euphorbiaceae; Oryzaeae; Oryza.
OX NCBI_TaxID=4530;
RN PROTEIN SEQUENCE.
RP Tsugita A.;
RL Submitted (APR-1993) to the PIR data bank.
CC -----
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-----
CC PIR; PS0249; PS0249.
DR Gramine; Q7MIU8; -.
FT NON_TER 1 1
SQ SEQUENCE 14 AA; 1490 MW; 83240AEOB1FAEA CRC64;

Query Match
Best Local Similarity 29.6%; Score 24; DB 2; Length 14;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 8 TDQYTTTG 15
DB 5 TDDHTANG 12

RESULT 6
O9S929_SOYBN PRELIMINARY; PRT; 15 AA.
AC O9S929;
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Pyruvate-5-carboxylate reductase, P5CR (Fragment).
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
OC Glycine.
OX NCBI_TaxID=3847;
RN (1)
RP PROTEIN SEQUENCE.
RA MEDLINE=91378472; PubMed=1898034;
RA Chilson O.P., Kelly-Chilson A.E., Siegel N.R.;
RT "Pyruvate-5-carboxylate reductase in soybean nodules:
RT isolation/partial primary structure/evidence for isozymes.";
RL Arch. Biochem. Biophys. 288:350-357 (1991).
CC -----
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CC -----
FT NON_TER 15
SQ SEQUENCE 15 AA; 1715 MW; D9821F73F3DF524 CRC64;

Query Match
Best Local Similarity 29.6%; Score 24; DB 2; Length 15;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 5 PIQTDQYT 12
DB 5 PIPEASYT 12

RESULT 7
ID PLMS_LAMNA STANDARD; PRT; 13 AA.
AC P83009;
DT 29-MAR-2005, integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-2001, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE Phospholemman-like protein (PLMS) (Fragment).
OS Lama naus (Goat) (Squalus naus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphi; Galeoidea; Lamniformes; Alopiidae;
OC Lama.
OX NCBI_TaxID=7849;
RN (1)
RP PROTEIN SEQUENCE.
RA TISSUE=Rectal gland;
RA MEDLINE=21534268; PubMed=11676495; DOI=10.1006/birc.2001.5826;
RA Schumann Stekhoven F.M.A.H., Flük G., Wendelaar Bonga S.E.;
RT "N-terminal sequences of small ion channels in rectal glands of

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RT sharks; a biochemical hallmark for classification and phylogeny?";
RL Biochem. Biophys. Res. Commun. 288:670-675(2001).
CC -1- FUNCTION: Induces a hyperpolarization-activated chloride current
CC when expressed in Xenopus oocytes. May have a functional role in
CC muscle contraction.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Mitochondrial
CC membrane.
CC -1- PTM: Major plasma membrane substrate for camp-dependent protein
CC kinase (PK-A) and protein kinase C (PK-C) in several different
CC tissues. Phosphorylated in response to insulin and adrenergic
CC stimulation (By similarity).
CC -1- SIMILARITY: Belongs to the FYXD family.
CC -----
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CC -----
DR GO:0005792; C:mitosome; IDA.
DR InterPro: IPR000272; FYXD.
DR PROSITE: PS01310; FYXD. PARTIAL.
KW Chloride; Chloride channel; Direct protein sequencing;
KW Endoplasmic reticulum; Ion transport; Ionic channel; Membrane;
KW Mitosome; Phosphorylation; Transmembrane; Transport.
FT CHAIN 1
FT /FTId=PRO_0000148181.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1542 MW; 081373C69724A44 CRC64;

Query Match
Best Local Similarity 28.4%; Score 23; DB 1; Length 13;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 2 NDSPIQTDQYT 12
DB 2 SDVPPNDRFT 12

RESULT 8
ID OLP_TOBAC STANDARD; PRT; 15 AA.
AC P80781;
DT 11-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DT 11-OCT-2005, sequence version 1.
DT 07-MAR-2006, entry version 5.
DE Osmotin-like protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN (1)
RP PROTEIN SEQUENCE. AND SUBCELLULAR LOCATION.
RA MEDLINE=97332671; PubMed=9188482; DOI=10.1074/jbc.272.25.15841;
RA Robertson D., Mitchell G.P., Gilroy J.B., Gerrish C., Botwell G.P.,
RA Slabas A.R.;
RT "Differential extraction and protein sequencing reveals major
RT differences in patterns of primary cell wall proteins from plants.";
RL J. Biol. Chem. 272:15841-15848(1997).
CC -1- SUBCELLULAR LOCATION: Cell wall.
CC -1- SIMILARITY: Belongs to the thaumatin family.
CC -----
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CC -----
DR InterPro: IPR001938; Thaumatin.
DR PROSITE: PS00316; THAUMATIN; PARTIAL.
KW Cell wall; Direct protein sequencing.
FT CHAIN 1
FT /FTId=PRO_0000096233.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1744 MW; 00030D70002A376B CRC64;

Query Match
Best Local Similarity 28.4%; Score 23; DB 1; Length 15;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RNDSP 5
Db 6 RNDSP 10

RESULT 9

09TVF1_TRYCR PRELIMINARY; PRT; 9 AA.
AC 09TVF1_TRYCR
DT 01-MAY-2000, integrated into UniProtKB/TrEMBL.
DT 01-MAY-2000, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE Mucin-like protein (Fragment).
GN Name=EMUC-19c8;
OS Trypanosoma cruzi.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma;
OC Schizotrypanum.
OX NCBI_TaxID=5693;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STAIN=C1-Brenner;
RX MEDLINE=98225151; PubMed=9556557; DOI=10.1074/jbc.273.18.10843;
RA Di Noia J.M., D'Oreco I., Aelund L., Sanchez D.O., Fraach A.C.;
RT "The Trypanosoma cruzi mucin family is transcribed from hundreds of
RT genes having hypervariable regions";
RL J. Biol. Chem. 273:10843-10850(1998).
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CC
CC EMBL: AF036447; AAC14246.1; -, mRNA.
FR NON_TER 1
SQ SEQUENCE 9 AA; 896 MW; DBA831B1B5DD72D CRC64;
Query Match 27.2%; Score 22; DB 2; Length 9;
Best Local Similarity 80.0%; Pred. No. 2.8e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 11 YTTTG 15
Db 5 YTTLG 9
RESULT 10
SC41_TITCA STANDARD; PRT; 10 AA.
AC P84684;
DT 25-OCT-2005, integrated into UniProtKB/Swiss-Prot.
DT 25-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Toxin Tc41 (Fragment).
OS Tityus cambridgei (Amazonian scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Buchida; Butioidae; Butiidae; Tityus.
OX NCBI_TaxID=184226;
RN [1]
RP PROTEIN SEQUENCE, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND MASS
RP SPECTROMETRY.
RC TISSUE=Venom;
RX PubMed=15025998; DOI=10.1016/j.jchromb.2003.09.002;
RA Batista C.V.F., del Pozo L., Zamudio F.Z., Contreras S., Becerril B.,
RA Manke B., Poeschl L.D.;
RT "Proteomics of the venom from the Amazonian scorpion Tityus cambridgei
RT and the role of prolines on mass spectrometry analysis of toxins";
RL J. Chromatogr. B 803:55-66(2004).
CC -1- SUBCELLULAR LOCATION: Secreted protein.
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -1- MASS SPECTROMETRY: MW=7109.4; METHOD=Electrospray; RANGE=1-7;
CC NOTE=Ref.1.
CC
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CC Direct protein sequencing; Toxin.
KW CHAIN 1 >10 Toxin Tc41.
FT FT /FTID=PRO_0000066806.
SQ SEQUENCE 10 AA; 1151 MW; 833166AAB3D77B5A CRC64;

Query Match 27.2%; Score 22; DB 1; Length 10;
Best Local Similarity 37.5%; Pred. No. 7.8e+03;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 RNDSP1QT 8
Db 1 KDDYFVD 8

RESULT 11

07IGS6_9HYME PRELIMINARY; PRT; 14 AA.
ID 07IGS6_9HYME
AC 07IGS6_9
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-MAR-2006, entry version 8.
DE Cytochrome oxidase subunit I (Fragment).
OS Andrena n. sp. 'goth'.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preyrgota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Andrenidae; Andreninae; Andrena; Callandrena.
OX NCBI_TaxID=205171;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=96;
RX PubMed=16343953; DOI=10.1016/j.ympev.2005.10.003;
RA Larkin L.V., Neft U.L., Simpson B.B.;
RT "Phylogeny of the Callandrena subgenus of Andrena (Hymenoptera:
RT Andrenidae) based on mitochondrial and nuclear DNA data: Polyphyly and
RT convergent evolution";
RL Mol. Phylogenet. Evol. 38:330-343 (2006).
CC
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CC
CC EMBL: AF504376; AAC07723.1; -, Genomic DNA.
DR GO: GO:0005739; C:mitochondrion; IEA.
KM Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1692 MW; 79E3B922A4E7BE5B CRC64;

Query Match 27.2%; Score 22; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 1.1e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NDSP1QT 8
Db 6 NEIPIMT 12

RESULT 12

054394_STRLI PRELIMINARY; PRT; 14 AA.
ID 054394_STRLI
AC 054394;
DT 01-NOV-1996, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 19.
DE S-adenosyl-L-homocysteine hydrolase (Fragment).
OS Streptomyces lividans.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomycetes.
OX NCBI_TaxID=1916;
RN [1]
RP NUCLEOTIDE SEQUENCE.

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RC STRAIN=TK21;
RA Romero N.M., Mellado R.P.;
RT "Activation of the actinorhodin biosynthetic pathway in Streptomyces
RL lividans.";
CC FEMS Microbiol. Lett. 1217:79-84(1995).
CC -----
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CC -----
CC EMBL; X79814; CA56211.1; -; Genomic DNA.
DR GO; GO:0004013; F:adenosylhomocysteinease activity; IEA.
DR GO; GO:0016787; F:hydrolyase activity; IEA.
DR GO; GO:0006730; P:one-carbon compound metabolism; IEA.
DR InterPro; IPR000043; Ad_hcy_hydrolyase.
DR Pfam; PF05221; AdoHcyase; 1.
KW Hydrolyase.
FT NON_TER
SQ SEQUENCE 14 AA; 1725 MW; 1303D5023C485D2B CRC64;

Query Match 27.2%; Score 22; DB 2; Length 14;
Best Local Similarity 33.3%; Pred. No. 1.1e+04;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 DSIPTDPOY 11
DB 4 EGPYKADHY 12

RESULT 13
UC19_MAIZE STANDARD; PRT; 15 AA.
AC P80625.
DT 01-OCT-1996, integrated into UniProtKB/Swiss-Prot.
DT 01-OCT-1996, sequence version 1.
DT 07-FEB-2006, entry version 21.
DE Unknown protein from 2D-PAGE of etiolated coleoptile (Spot 406
DE (Fragment)).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OC NCBI_TaxID=4577;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Coleoptile;
RA Touzet P., Ricciardi F., Morin C., Damerval C., Hueb J.-C.,
RA Pernollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated
RT genome analysis program.";
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 5.6, its MW is: 18.4 kDa.
CC -----
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CC -----
CC Gramine; P80625; -;
DR MaizEDB; 123951; -;
KM Direct protein sequencing.
FT CHAIN
FT FT <1 >15
FT FT Unknown protein from 2D-PAGE of etiolated
FT FT coleoptile.
FT FT /FTID=PRO_0000055515.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 15 AA; 1672 MW; 1CF69D4DA8737F9D CRC64;

Query Match 27.2%; Score 22; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.2e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 QYTTTG 15
DB 4 RYTTYG 9

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RESULT 14
ID Q71G6_9HYME PRELIMINARY; PRT; 15 AA.
AC Q71G6_9HYME
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-MAR-2006, entry version 9.
DE Cytochrome oxidase subunit I (Fragment).
OS Andrena simulata.
OC Andrena.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preyrgota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Apoidea;
OC Andrenidae; Andreninae; Andrena; Callandrena.
OC NCBI_TaxID=205253;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=104;
RX PubMed=16343953; DOI=10.1016/j.ympev.2005.10.003;
RA Larkin L.U., Neft U.L., Simpson B.B.;
RT "Phylogeny of the Callandrena subgenus of Andrena (Hymenoptera:
RT Andrenidae) based on mitochondrial and nuclear DNA data: Polyphly and
RT convergent evolution.";
RL Mol. Phylogenet. Evol. 38:330-343(2006).
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CC -----
CC EMBL; AF504361; AA007693.1; -; Genomic DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 15 AA; 1744 MW; 181E812922A4F3EE CRC64;

Query Match 27.2%; Score 22; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 1.2e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 NDSPLOT 8
DB 6 NEPIPT 12

RESULT 15
ID Q71H38_9HYME PRELIMINARY; PRT; 15 AA.
AC Q71H38_9HYME
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 07-MAR-2006, entry version 9.
DE Cytochrome oxidase subunit I (Fragment).
OS Andrena auripes.
OC Andrena.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preyrgota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Apoidea;
OC Andrenidae; Andreninae; Andrena; Callandrena.
OC NCBI_TaxID=205215;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=126;
RX PubMed=16343953; DOI=10.1016/j.ympev.2005.10.003;
RA Larkin L.U., Neft U.L., Simpson B.B.;
RT "Phylogeny of the Callandrena subgenus of Andrena (Hymenoptera:
RT Andrenidae) based on mitochondrial and nuclear DNA data: Polyphly and
RT convergent evolution.";
RL Mol. Phylogenet. Evol. 38:330-343(2006).
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CC -----
CC EMBL; AF504320; AA007611.1; -; Genomic DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.

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KW Mitochondrion. 1
FT NON TER 1
SQ SEQUENCE 15 AA; 1776 MW; 09EE90D922A4EE59 CRC64;
Query Match 27.2%; Score 22; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 1.2e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 2 NDSP1QT 8
| : |||
Db 6 NEIP1MT 12

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